

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____

Art. Unit: _____ Phone Number 30 _____ Serial Number: _____

Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER-DISK-E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers; and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: <u>John</u>	Searcher Phone #: <u>4448</u>	NA Sequence (#) <u>2</u>	STN _____
Searcher Location: _____	Date Searcher Picked Up: <u>11/5</u>	AA Sequence (#) <u>6</u>	Dialog _____
Date Completed: <u>11/13</u>	Searcher Prep & Review Time: _____	Structure (#) _____	Questel/Orbit _____
Clerical Prep Time: <u>20</u>	Patent Family _____	Bibliographic _____	Dr.Link _____
Online Time: <u>+15</u>	Other _____	Litigation _____	Lexis/Nexis _____
		Fulltext _____	Sequence Systems <u>✓</u> _____
		Other _____	WWW/Internet _____
			Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: November 9, 2001, 15:30:16 ; Search time 79.75 seconds
(without alignments)
161.917 Million cell updates/sec

Title: US-09-668-021-2

Perfect score: 213

Sequence: 1 MOLFIAALCLVCLVHTAFLRV KPRPRPARSAKANDAELENAY 213

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Purchased: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_0601:*

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20: /SIDS8/gcdata/geneseq/geneseq/geneseq/AA2000.DAT: *
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ALIGNMENTS

RESULT	1
ID	ARB26106
DE	ARB26106 standard; Protein; 213 AA.
AC	ARB26106;
DT	15-JAN-2001 (first entry)
XX	Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and 4).
XX	Human; DNA/Cerberus-related protein 6; hDCR6; morphogenetic protein; antagonist; BMP; cell growth; cell differentiation; bone formation; gene therapy.
XX	
OS	Homo sapiens.
OS	
PN	W0200055193-A2.
XX	
PD	21-SEP-2000.
XX	
PF	02-MAR-2000; 2000W0-US05537.
XX	
PR	12-MAR-1999; 90US-0124118.
XX	
RA	(REGE-) REGENERON PHARM INC.
XX	
PI	Economides AN;
XX	
DR	WPI; 2000-638179/61.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	213	100.0	213	21	ARB26106	Human DAN/Cerberus
2	213	100.0	213	21	AYY96429	Human TGF-beta bin
3	100.0	213	22	AYY97389	Human secreted pro	
4	82.2	213	21	AYY96430	Human TGF-beta bin	
5	82.2	213	21	AYY96436	Human TGF-beta bin	
6	65.3	367	21	ARB26105	Human DAN/Cerberus	
7	63.4	213	21	AYY96431	Vervet TGF-beta bin	
8	35.7	176	21	AYY9634	Bovine TGF-beta bin	
9	23.0	50	20	AYY12009	Human 5' EST score	
10	15.5	213	21	AYY96433	Human TGF-beta bindi	
11	15.0	211	21	AYY96432	Murine TGF-beta bin	

DR	N-PSDB; AAA94051.	PT	Nucleic acids {1} encoding a transforming growth factor beta binding
XX		PT	protein, useful for identifying agents for treating osteopenia,
PT	Novel isolated, human DNA/Cerberus related protein 6 which include	PT	osteoporosis and fractures
PT	natural homologue, and polypeptides comprising DCR6 domain and nucleic	XX	
PT	acids encoding the proteins which are useful as probes and primers	PS	
XX		XX	Claim 2; Page 116; 162PP; English.
PS		CC	The present sequence comprises the amino acid sequence encoded by exons 1
Claim 8; Fig 3; 40pp; English.	CC	CC	and 4 of the human DAN/Cerberus related protein 6 (hDCR6) coding
CC	CC	CC	sequence. The coding sequence was isolated from a human kidney cDNA
CC	CC	CC	library containing exons 1 and 4 of the sequence. hDCR6 is closely
CC	CC	CC	related to the DAN and DCX5 proteins, both of which act as antagonists of
CC	CC	CC	morphogenic proteins such as BMP. It is possible that the hDCR6 gene and
CC	CC	CC	protein can be used as immunogens, modulators of cell function, growth
CC	CC	CC	and differentiation, to reduce undesirable bone formation, to identify
CC	CC	CC	DCR6 binding agents, in diagnosis, and in gene therapy.
XX	Sequence	CC	CC
XX	213 AA;	CC	CC
Query Match	100.0%; Score 213; DB 21; Length 213;	CC	CC
Best Local Similarity	100.0%; Pred. No. 2.1e-212;	CC	CC
Matches	213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC
Qy	1 MQLPIALCIVCLVLTAFVVEGQWQAFKNDATEIPELGEYPPPELENKTMRAE	CC	CC
Db	1 mqplialcivclvltafvveggwafkndateiipeleypppeilenktnrae	CC	CC
Qy	61 NGGRPHPHPETKDVSEYSCRELFHTRVTDPCRSAKPVTELVSQGCQCPARLPMAG	CC	CC
Db	61 nggrphphpetkdvseysscrelfhtrvtdpcrsakpvtelvsqgcparlpmag	CC	CC
Qy	121 RGKWRPSPGDFRCTPDRYRAQRVQLCQPGGEAPRARKVRLYASCKCRTRFHNOSEK	CC	CC
Db	121 rgkwrsppgdfrcipdrtyraqvqlcqpggeaprkvrivaskcktrtrfhnselk	CC	CC
Qy	181 DFGTEAARPKGRKPRRASAKANQALENAY 213	CC	CC
Db	181 dfgtearpkgrkprraskanqaleney 213	CC	CC
RESULT	2	CC	CC
ID	AAV96429	CC	CC
XX	AAV96429 standard; Protein; 213 AA.	CC	CC
AC	AAV96429;	CC	CC
XX		CC	CC
DT	12-SEP-2000 (first entry)	CC	CC
XX		CC	CC
EE	Human TGF-beta binding protein (BEER).	CC	CC
XX		CC	CC
KW	osteopathic; transforming growth factor-beta; TGF-beta; binding protein;	CC	CC
KW	BEER; gene therapy; antisense therapy; fracture; bone mineralization.	CC	CC
XX		CC	CC
OS	Homo sapiens.	CC	CC
XX		CC	CC
WO20032773-A1		CC	CC
PD	08-JUN-2000.	CC	CC
XX		CC	CC
PP	24-NOV-1999; 99W0-US27990.	CC	CC
XX		CC	CC
PR	27-NOV-1998; 98US-010283.	CC	CC
XX		CC	CC
PA	(DARW-) DARWIN DISCOVERY LTD.	CC	CC
XX		CC	CC
PI	Brunckow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepke BW;	CC	CC
PI	Van Ness J, Winkler DG;	CC	CC
XX		CC	CC
DR	WPI; 2000-412301/35.	CC	CC
XX		CC	CC
N-PSDB; AAA29055.		CC	CC
Query Match	100.0%; Score 213; DB 21; Length 213;	CC	CC
Best Local Similarity	100.0%; Pred. No. 2.1e-212;	CC	CC
Matches	213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC
Qy	1 MQLPIALCIVCLVLTAFVVEGQWQAFKNDATEIPELGEYPPPELENKTMRAE	CC	CC
Db	1 mqplialcivclvltafvveggwafkndateiipeleypppeilenktnrae	CC	CC
Qy	61 NGGRPHPHPETKDVSEYSCRELFHTRVTDPCRSAKPVTELVSQGCQCPARLPMAG	CC	CC
Db	61 nggrphphpetkdvseysscrelfhtrvtdpcrsakpvtelvsqgcparlpmag	CC	CC
Qy	121 RGKWRPSPGDFRCTPDRYRAQRVQLCQPGGEAPRARKVRLYASCKCRTRFHNOSEK	CC	CC
Db	121 rgkwrsppgdfrcipdrtyraqvqlcqpggeaprkvrivaskcktrtrfhnselk	CC	CC
Qy	181 DFGTEAARPKGRKPRRASAKANQALENAY 213	CC	CC
Db	181 dfgtearpkgrkprraskanqaleney 213	CC	CC
RESULT	3	CC	CC
ID	AAV97589	CC	CC
XX	AAV97589 standard; Protein; 213 AA.	CC	CC
AC	AAV97589;	CC	CC
XX		CC	CC
DT	05-APR-2001 (first entry)	CC	CC
XX		CC	CC
DE	Human secreted protein PRO7476.	CC	CC
XX		CC	CC
KW	Secreted protein; human; PRO protein; neoplastic cell growth; tumour;	CC	CC
KW	proliferation; leukaemia; lymphoid malignancy; inflammatory disorder;	CC	CC
KW	angiogenic disorder; immunologic disorder; PRO7476.	CC	CC
XX		CC	CC
OS	Homo sapiens.	CC	CC
XX		CC	CC
WO20075317-A2		CC	CC
PD	14-DEC-2000.	CC	CC
XX		CC	CC
PP	15-MAY-2000; 2000WO-US13358.	CC	CC
XX		CC	CC
PR	09-JUN-1999; 99US-0138385.	CC	CC
PR	20-JUL-1999; 99US-014790.	CC	CC
PR	03-AUG-1999; 99US-0146843.	CC	CC
PR	10-AUG-1999; 99US-0148188.	CC	CC
PR	17-AUG-1999; 99US-019320.	CC	CC

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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 21:20:08 ; Search time 6020.71 Seconds
 (without alignments)
 5911.477 Million cell updates/sec

Title: US-09-668-021-1
 perfect score: 2301
 Sequence: 1 agagctgtgtactggaaag.....caatgaatcatgaccgaaag 2301
 Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

searched: 1344157 seqs, 7733874588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database	Summary
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2301	100.0	2323	89 AF326739	AF326739 Homo sapi
2	2230	96.9	2329	9 AF056687	AF056687 Sequence
3	2163	96.9	2296	89 AF331844	AF331844 Homo sapi
4	2036	88.5	21501	89 AF326736	AF326736 Homo sapi
5	2036	88.5	94752	85 AC003098	AC003098 Homo sapi
6	1915	83.2	15780	72 AC055813	AC055813 Homo sapi
7	661	28.7	177744	75 AC077954	AC077954 Homo sapi
8	10.0	177744	75 AC077954	83 AC077954	AC077954 Homo sapi

FEATURES		Submitted (07-DEC-2000)	Genomics, Celltech Chiroscience Inc.	1631
source		220th St. SE, Bothell, WA 98021, USA		
AC056701	Sequence	1.	2.323	
AC008708	Homo sapi	1.		
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AC021288	Zebrafish			
AC090133	Mus muscu			
AC068807	Mus muscu			
AC0326741	Rattus no			
AC056701	Sequence	1.	47	
AC008708	Homo sapi	1.	47	
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AC021288	Zebrafish			
AC090133	Mus muscu			
AC011261	Homo sapi			
AC058140	Homo sapi			
AC0590642	Homo sapi			
AC0590642	Zebrafish			
AC0533761	Homo sapi			
AC067756	Homo sapi			
AC011308	Homo sapi			
AC080073	Homo sapi			
AC078582	Human DNA			
AC079791	Homo sapi			
AL139008	Human DNA			
AL139008	Homo sapi			
AL450401	Homo sapi			
AC074100	Homo sapi			
AL356439	Homo sapi			
AL356093	Human DNA			
AL356093	Homo sapi			
AF029308	Homo sapi			
AF312033	Mus muscu			
AF114775	Ictalurus			
Z16819	H. sapiens			
G39626	Zebrafish			
G39626	26994			
AJ243714	cryptotis			
AF314679	Deltopterus			
AF189701	Biomphala			
G39227	Zebrafish			
AF199380	Mus muscu			
AJ251155	Mus muscu			
AL390210	Human DNA			
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BASE COUNT	590	a	635	c
ORIGIN				
1	47			
48	.689			
49				
50				
ALIGNMENTS				
RESULT	1			
AF326739	AF326739	2233 bp	mRNA	PRI
ACUS	ACUS			
DEFINITION	Homo sapiens sclerostin mRNA, complete cds.			
ACCESSION	AF326739			
VERSION	1			
KEYWORDS	GI:13161019			
SOURCE	human			
ORGANISM	Homo sapiens			
Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 2323)				
REFERENCE				
AUTHORS	Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, D., Hamersma, H., Brighton, P., and Mulligan, J.T.			
TITLE	Bone Dysplasia Sclerostosis Results from Loss of the SOST Gene Product, a Novel Cystine Knot-Containing Protein			
JOURNAL	Am. J. Hum. Genet. 68 (3), 577-589 (2001)			
PUBLISHED	11/17/2006			
REFERENCE	2 (bases 1 to 2323)			
AUTHORS	Brunkow, M.E., Gardner, J.C., Van Ness, J., Paeper, B.W., Kovacevich, B.R., Proll, S., Skonier, J.E., Zhao, L., Sabo, P.J., Fu, Y.H., Alisch, R.S., Gillett, L., Colbert, T., Tacconi, P., Galas, D., Hamersma, H., Brighton, P., and Mulligan, J.T.			
TITLE	Direct Submission			

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2001, 01:07:51 ; Search time 6020.71 Seconds
(without alignments)
5911.477 Million cell updates/sec

Title: US-09-668-021-5
Perfect score: 2301
Sequence: 1 agaggctgtgtacttggaaag.....caatgaatcatcatgaccgaaag 2301
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Word size : 0
arched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 50 summaries
Database : GenEmbl:
1: gb_ba1:
2: gb_ba2:
3: gb_ba3:
4: gb_in1:
5: gb_in2:
6: gb_in3:
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8: gb_ov:
9: gb_patt1:
10: gb_patt2:
11: gb_ph:
12: gb_p11:
13: gb_p12:
14: gb_p13:
15: gb_p14:
16: em_ba1:
17: em_ba2:
18: em_fun:
19: em_htg0_hum:
20: em_htg0_inv:
21: em_htg0_rdi:
22: em_htg_hum1:
23: em_htg_hum2:
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25: em_htg_hum4:
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40: em_hum7:
41: em_in:
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43: em_in:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2199	95.6	2323 89 AF326739	AF326739 Homo sapi AX05687 Sequence
2	2128	92.5	2329 9 AF326739	AF326736 Homo sapi AF331844 Homo sapi
3	2061	89.6	2296 89 AF326736	AF326736 Homo sapi AF331844 Homo sapi
4	2036	88.5	2150 89 AF326736	AF326736 Homo sapi AF331844 Homo sapi
5	1915	83.2	151780 72 AC055813	AC055813 Homo sapi AC073954 Homo sapi AC073954 Homo sapi
6	661	84.7	177744 75 AC073954	AC073954 Homo sapi AC073954 Homo sapi
7	661	84.7	177744 75 AC073954	AC073954 Homo sapi AC073954 Homo sapi
8	201	84.7	177744 75 AC073954	AC073954 Homo sapi AC073954 Homo sapi

8

Run on: November 10, 2001, 00:15:05 ; Search time 272.77 seconds
OM nucleic - nucleic search, using sw model
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GenCore Version 4.5

Word size : 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

database : N_Geneseq_0601:*

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12: /$IDS8/ggdata/geneseq/geneseq/NA1991.DAT
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22: /$IDS8/ggdata/geneseq/geneseq/NA2001.DAT
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Score, n , is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

NO.	Score	Vscore	Length	DB	ID	Description
1	2301	100.0	2301	21	AAAG29056	Human TGF-beta bin
2	2250	97.8	2301	21	AAAG29062	Human TGF-beta bin
3	2199	95.6	2301	21	AAAG29055	Human TGF-beta bin
4	2148	93.4	2301	21	AAAG29051	Mutant human TGF-beta bin
5	2128	92.5	2329	22	AAAG19123	Human secreted protein
6	2036	88.5	5680	21	AAAG40449	Human DAN/Cerberus
7	2036	88.5	9301	21	AAAG29064	Human TGF-beta bin
8	563	24.5	642	21	AAAG94051	Human DAN/Cerberus
9	422	18.3	1104	21	AAAG4050	Human DAN/Cerberus
10	108	4.7	198	21	AAAC05741	Human secreted protein
11	108	4.7	198	20	AAAC0842	Human secreted protein

12	92	4.0	642	21	AAQ9057	Vervet TGF-beta bi
13	83	4.0	642	21	AAQ9057	Bovine TGF-beta bi
14	69	3.0	638	21	AAQ29058	Murine TGF-beta bi
15	69	3.0	35828	21	AAQ29063	Murine TGF-beta bi
16	68	3.0	674	21	AAQ29059	Rat TGF-beta bindi
17	40	1.7	40	22	AAQ91036	Probe for Human se
18	28	1.2	39	21	AAQ34042	Human HDCR6 exon 1
19	27	1.2	27	22	AAQ91035	PCR primer for Hum
20	27	1.2	38	21	AAQ94048	Human HDCR6 exon 4
21	27	1.2	1303	21	AAC19909	Human secreted pro
22	26	1.1	30	21	AAQ94047	Human HDCR6 exon 4
23	26	1.1	49	13	AAQ33591	Microsatellite seq
24	26	1.1	320	20	AAX74405	Rat U3 gene trap d
25	26	1.1	355	21	AAQ31528	Rat microsatelli
26	26	1.1	421	21	AAQ80642	Human secreted pro
27	26	1.1	559	21	AAC5918	Eucalyptus grandis
28	26	1.1	597	16	AAQ95193	Simple tandem repe
29	26	1.1	893	16	AAQ92529	P. communis (pear)
30	26	1.1	1568	21	AAC37436	Arabidopsis thalia
31	26	1.1	2295	21	AAQ86010	Human CD33-like se
32	26	1.1	2483	17	AAT45982	Human cocaine and
33	26	1.1	2483	19	AAT57895	Human cocaine and
34	26	1.1	2483	20	AAZ25566	Human cocaine and
35	26	1.1	2764	20	AAX34109	Human PRO940 nucle
36	26	1.1	2764	21	AATC7510	Human PRO940 (UNQ4
37	26	1.1	2919	18	AAT1124	Human homeoprotein
38	26	1.1	3099	20	AAY99912	Human sialoadhesin
39	26	1.1	3099	20	AAY99912	Human sialoadhesin
40	26	1.1	3515	22	AAF75343	Human TGF-beta rec
41	26	1.1	4011	20	AAX60124	DNA sequence of th
42	26	1.1	4315	21	AAE6021	Maize Krox11 prom
43	26	1.1	6083	21	AAN31398	Chromosome 16q tum
44	26	1.1	7715	19	AAY43042	Mus musculus Cgamm
45	26	1.1	8760	15	AQ73473	Porcine pro-interl
46	26	1.1	9840	22	AAQ85482	Murine neuropeptid
47	26	1.1	16442	18	AAY83006	Partial mouse WRN
48	26	1.1	23241	22	AAY97387	Human neuroblastom
49	26	1.1	23241	22	AAE97871	Human neuroblastom
50	26	1.1	49999	20	AAZ233895	Murine LOBO homolo

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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 21:18:58 ; Search time 3376.69 Seconds

(without alignments) 6441.520 Million cell updates/sec

Title: US-09-668-021-1
 Perfect score: 2301
 Sequence: 1 agagctgtgtctactggaaag.....caatgaatcatgaccgaaag 2301
 Scoring table: Oligo_NUC
 Gapop 60.0 , Gapext 60.0
 Searched: 10228115 seqs, 4726426750 residues
 Word size : 0
 Total number of hits satisfying chosen parameters: 20456230
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: listing first 50 summaries
 Database : EST:
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 2: gb_est2: *
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 4: gb_est4: *
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 7: gb_est7: *
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 9: gb_est9: *
 10: gb_est10: *
 11: gb_est11: *
 12: gb_est12: *
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117: qb_est48:*
118: qb_est49:*
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251: qb_gss34:*
252: em_gss_inv4:*
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254: em_gss_rnd7:*
255: em_gss_rnd8:*
256: qb_gss35:*
257: qb_gss36:*
258: qb_gss37:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 21:26:53 ; Search time 272.77 seconds
(without alignments) 5296.776 Million cell updates/sec

Title: US-09-668-021-1

Perfect score: 2301

Sequence: 1 agaacctgtgtacttggaa.....caataaatcatgacccgaaag 2301

Scoring table: Oligo-NUC Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : N_Genesed_0601:*

1: /\$IDS8/gcdata/genesed/geneseq/geneseq/N1980.DAT:*

2: /\$IDS8/gcdata/genesed/geneseq/geneseq/N1981.DAT:*

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21: /\$IDS8/gcdata/geneseq/geneseq/N2001.DAT:*

22: /\$IDS8/gcdata/geneseq/geneseq/N2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2301	100.0	2301	Human TGF-beta bin
2	2250	97.8	2301	Mutant human TGF-beta bin
3	2250	97.8	2301	Human TGF-beta bin
4	2230	96.9	2329	Human secreted pro
5	2199	95.6	2301	Human TGF-beta bin
6	2036	88.5	5680	Human TGF-beta bin
7	88.5	9301	21	Human TGF-beta bin
8	642	27.9	642	Human TGF-beta bin
9	422	18.3	1104	Human TGF-beta bin
10	193	8.4	196	Human secreted pro
11	193	8.4	198	Human secreted pro

ALIGMENTS

RESULT	1
ID	AAA29055 standard; cDNA; 2301 BP.
AC	AAA29055;
XX	
DT	12-SEP-2000 (first entry)
DE	Human TGF-beta binding protein (BEER) cDNA.
KW	osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; chromosome 17q12-21; gene therapy; antisense therapy; fracture; bone mineralization; ss.
OS	Human sapiens.
XX	
FF	
Key	
CDS	
FT	
FT	
FT	
XX	
PN	W0200032773-A1.
XX	
PD	08-JUN-2000.
XX	
PF	24-NOV-1999;
XX	
PR	27-NOV-1998;
XX	

vervet TGF-beta bi
Bovine TGF-beta bi
Murine TGF-beta bi
Rat TGF-beta bindi
Probe for Human se
Human hDCR6 exon 1
Human hDCR6 exon 1
PCR primer for Hum
Human hDCR6 exon 4
Human secreted pro
Human hDCR6 exon 4
Microsatellite seq
Rat U3 gene trap d
Plant microsatelli
Human secreted pro
Eucalyptus grandis
Simple tandem repe
P. communis (pear)
Arabidopsis thalia
Human CD33-like se
Human cocaine and
Human PRO940 nucle
Human PRO940 (In04
Human homeoprotein
Human sialoadhesin
Human TGF-beta rec
DNA sequence of th
Maize Knox1 promot
Chromosome 16Q tum
Mus musculus Cgamm
Porcine prointerl
Murine neuropeptid
Partial mouse wrn
Human neuroblastom
Human neuroblastom

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Om nucleic - nucleic search, using sw model

Run on: November 9, 2001, 21:24:43 ; Search time 134.61 seconds
(without alignments)

3871.376 Million cell updates/sec

Title: US-09-668-021-1
Perfect score: 2301
Sequence: 1 agagctgtctactgaaag.....caatgaatcatgaccgaaag 2301

Scoring table: OLIGO_NUC
Gappop 60.0 , Gapext 60.0

Word size : 0

351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_NA:*

1: /cgn2_5/ptodata/1/ina/5K_COMB.seq: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PC1US_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGMENTS

RESULT 1
US-08-332-766A-19
; Sequence 19, Application US/08332766A
; PATENT NO. 5843647
; GENERAL INFORMATION:
; APPLICANT: JEFFREYS, Alec J.
; APPLICANT: ARMOUR, John
; TITLE OF INVENTION: SIMPLE TANDEM REPEATS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-5918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,766A
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326052.9
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BIRD, Donald J.
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 21721/M94/0434/GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-332-766A-19

Query Match 1.1%; Score 26; DB 2; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0.014; Indels 0;
 Matches 26; Conservative 0; Mismatches 0; Gaps 0;

Qy 1328 gagagagagagagagagagaga 1353
 Db 399 GAGAGAGAGAGAGAGAGAGA 424

RESULT 2

US 08-276-452A-65/C

Sequence 66, Application US/08276452A

Patent No. 5646029

GENERAL INFORMATION:

APPLICANT: Chen, Chao-Guang

APPLICANT: Mau, Shiao-Lim

APPLICANT: Du, He

APPLICANT: Gane, Alison M

APPLICANT: Bacic, Antony E

APPLICANT: Clarke, Adrienne E

TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/276,452A

FILING DATE: 18-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Caruthers, Jennie M.

REGISTRATION NUMBER: 34,464

REFERENCE/DOCKET NUMBER: 27-91A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)499-8080

TELEFAX: 49617824

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 893 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 70..504

FEATURE:

NAME/KEY: misc_feature

LOCATION: 70..138

LOCATION: 70..138

OTHER INFORMATION: /note= "Putative secretion signal

OTHER INFORMATION: peptide"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 70..339

OTHER INFORMATION: /note= "Amino acids 70-138, 38-53, and 71-90 are sequences which match the peptide

OTHER INFORMATION: sequences obtained by protein sequencing"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 87..324

OTHER INFORMATION: /note= "Amino acids 40, 44, 45, 49, and 71-90 are sequences which match the peptide

OTHER INFORMATION: 50, 74, 76, 80, 81, and 85 are hydroxylated

RESULT 3

US-08-798-744-66/C

Sequence 66, Application US/08798744

Patent No. 5830747

GENERAL INFORMATION:

APPLICANT: Chen, Chao-Guang

APPLICANT: Mau, Shiao-Lim

APPLICANT: Du, He

APPLICANT: Gane, Alison M

APPLICANT: Bacic, Antony E

APPLICANT: Clarke, Adrienne E

TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee and Winner, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/798,744

FILING DATE: 13-FEB-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/276,452

FILING DATE: 18-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Caruthers, Jennie M.

REGISTRATION NUMBER: 34,464

REFERENCE/DOCKET NUMBER: 27-91A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303)499-8080

TELEFAX: 49617824

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 893 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 70..504

FEATURE:

NAME/KEY: misc_feature

LOCATION: 70..138

OTHER INFORMATION: /note= "Putative secretion signal

OTHER INFORMATION: peptide"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 70..339

OTHER INFORMATION: /note= "Amino acids 70-138, 38-53, and 71-90 are sequences which match the peptide

OTHER INFORMATION: sequences obtained by protein sequencing"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 87..324

OTHER INFORMATION: /note= "Amino acids 40, 44, 45, 49, and 71-90 are sequences which match the peptide

OTHER INFORMATION: 50, 74, 76, 80, 81, and 85 are hydroxylated

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 22:25:30 ; Search time 3375.69 Seconds
 (without alignments)
 6441.520 Million cell updates/sec

Title: US-09-668-021-5
 Perfect score: 2301
 Sequence: 1 agagcctgtgacttggaa...caatgaatcatgaccgaaag 2301

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 0

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

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255: em_gss_r0d6;*
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257: gb_gss36;*
258: gb_gss37;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match	Length	DB	ID	Description
1	8	3.8	428	1	TVHUEK		transforming prote
2	8	3.8	429	2	JC1965		elk1 protein - mouse
3	7	3.3	130	2	D83305		hypothetical prote
4	7	3.3	148	2	C83091		hypothetical prote
5	7	3.3	183	2	B37410		H-2 class II histo
6	7	3.3	197	2	G81057		hypothetical prote
7	7	3.3	197	2	A81819		hypothetical prote
8	7	3.3	305	2	S77397		yabc protein - homolog
9	7	3.3	312	2	D75444		conserved hypoth
10	7	3.3	321	2	BB2892		conserved hypoth
11	7	3.3	328	2	S72647		hypothetical prote
12	7	3.3	398	1	S24402		polyferredoxin 6x2
13	7	3.3	408	2	D70365		filibrillar assembly
14	7	3.3	412	1	KHHID		cathepsin D (EC 3.
15	7	3.3	510	2	S62901		legumin 31 precurs
16	7	3.3	512	1	WMCYFMM		inclusion body mat
17	7	3.3	562	2	T05758		hypothetical prote
18	7	3.3	587	2	T16617		NADH dehydrogenase
19	7	3.3	602	2	S47880		surface glycoprote
20	7	3.3	632	1	VGVNSY		outer membrane hem
21	7	3.3	681	2	E82812		protein kinase dra
22	7	3.3	781	1	TVFFDF		hexokinase (EC 2.7
23	7	3.3	917	1	S15885		hypothetical prote
24	7	3.3	946	2	T16297		nyosin in heavy chain
25	7	3.3	1940	2	A59387		polyketide synthas
26	7	3.3	6420	2	T30283		neurotoxin Tx2 - S
27	6	2.8	49	2	S29215		maix protein - Kle
28	6	2.8	65	2	B25125		tightly associated
29	6	2.8	83	2	S41672		

Gene 174, 185-188, 1996
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: CB1091
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; L
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 i; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337
 A;Accession: CB1091
 A;Title: Net: a new ets transcription factor that is activated by Ras.
 A;Reference number: A53037; MUID:95047310
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 A;Gene: elkl
 A;Introns: 70/3; 219/3; 363/3; 397/3
 C;Superfamily: elkl-1 transforming protein; ets DNA-binding domain homology
 E;7-86/Domain: ets DNA-binding domain homology <ETS>
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 B37410
 H-2 class II histocompatibility antigen A-2 beta chain - spiny mouse (Mus saxicola) (Mus
 C;Species: Mus saxicola
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 R;Cam, P.; Jouvin-Marche, E.; LeGuern, C.; Marche, P.N.
 Bur. J. Immunol. 20, 1337-1343, 1990
 A;Title: Structure of class II genes in wild mouse Mus saxicola: functional and evolutionary
 A;Reference number: A37410; MUID:90316177
 A;Accession: B37410
 A;Status: preliminary
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 Db 311 PQKGRKPR 318
 RESULT 3
 D83305
 hypothetical protein PA2722 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Accession: D83305
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 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; L
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 i; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
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 A;Experimental source: strain PA01
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 C;Species: *Neisseria meningitidis*
 C;Accession: G81057
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, B.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Piazza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
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 C83091
 hypothetical protein DAAA1 [imported] - *Pseudomonas aeruginosa* (strain PA01)
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 C;Accession: C83091
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 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 i; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
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 A;Experimental source: strain PA01
 A;Gene: PA2722
 RESULT 4
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 C;Species: *Pseudomonas aeruginosa*
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 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; L
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 i; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
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Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5				
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Sequence:	(without alignments) 235.141 Million cell updates/sec				
Scoring table:	OLIGO				
Gapop 60.0 , Gapext 60.0					
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Total number of hits satisfying chosen parameters:	93435				
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Maximum DB seq length:	2000000000				
Post-processing:	Listing first 50 summaries				
Database :	SwissProt_39:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
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2	8	3.8	429	1	ELK1_MOUSE
3	7	3.3	110	1	RL22_LEPN
4	7	3.3	305	1	YB44_SYN13
5	7	3.3	412	1	CATD_HUMAN
6	7	3.3	512	1	IBMP_FMVD
7	7	3.3	602	1	NUSM_DIDMV
8	7	3.3	632	1	VGLG_SYN4
9	7	3.3	781	1	KRAF_DROME
10	7	3.3	917	1	HAK2_MOUSE
11	7	3.3	917	1	HAK2_RAT
12	6	2.8	49	1	TX25_PHONT
13	6	2.8	65	1	MAXA_KLEP
14	6	2.8	97	1	OSTC_CHICK
15	6	2.8	97	1	VE7 HPV44
16	6	2.8	101	1	AC2_MACFA
17	6	2.8	110	1	RL22_ECOLI
18	6	2.8	111	1	RL22_ACHLA
19	6	2.8	112	1	RL22_SPIC1
20	6	2.8	113	1	RL22_THETHI
21	6	2.8	115	1	TIAF_HUMAN
22	6	2.8	115	1	TIAF_MOUSE
23	6	2.8	118	1	REV_HVILW
24	6	2.8	123	1	RS12_ECOLI
25	6	2.8	131	1	RL22_PYF51
26	6	2.8	135	1	RL4_BOVIN
27	6	2.8	135	1	RL4_CAPTH
28	6	2.8	135	1	RL4_SHEEP
29	6	2.8	146	1	YIK_ECOLI
30	6	2.8	150	1	R19E_PYRHO
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RT	"elk1", tissue-specific ets-related genes on chromosomes X and 14 near translocation breakpoints";				
RL	Science 244:66-70(1989).				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=99013876; PubMed=9795224;				
RX	Hariharan N., Mills F.C., Mitchell M.P., Meindl A., Max E.E.,				
RT	"The human elk-1 gene family: the functional gene and two processed pseudogenes embedded in the IgH locus.";				
RL	Gene 221:215-224(1998).				
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RA	Graham D.;				
RL	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.				
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RA	Aryee D.N.T., Kovar H.;				
RT	"Novel family members HUE271, ELF8, and ELKV among ETS-related genes coexpressed with EWS-FLI1 in Ewing tumor cell lines.";				
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RA	MEDLINE=92334979; PubMed=1630903;				
RT	"Elk-1" protein domains required for direct and SRP-assisted DNA-binding.";				
RT	Nucleic Acids Res. 20:3317-3324(1992).				
CC	-i- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA				
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CC	FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE				
CC	ELEMENT.				
CC	-i- SUBCELLULAR LOCATION: NUCLEAR.				
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE					
Q02326 saccharomyces					

CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: LUNG AND TESTIS.
 CC -!- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
 CC AND ERK).
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC
 CC DR PIR: A41354; TWHCK.
 CC DR HSSP: P14921; 2STW.
 CC DR TRANSPAC; T00250; -.
 CC DR MIM: 311040; -.
 CC DR InterPro: IPR000418; -.
 CC DR Pfam: PF00178; Ets; 1.
 CC DR PRINTS; PRO00454; ETS_DOMAIN.
 CC DR PROSITE; PS00346; ETS_DOMAIN; 2; 1.
 CC DR PROSITE; PS50031; ETS_DOMAIN; 3; 1.
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 Qy 189 PQKGKPR 196
 Db 310 PQKGKPR 317
 CC
 CC RESULT 2
 CC EKL_MOUSE STANDARD; PRT; 429 AA.
 CC ID EKL_MOUSE
 CC P41959; 01-NOV-1995 (Rel. 32, Created)
 CC 01-OCT-1996 (Rel. 34, last sequence update)
 CC 15-JUL-1999 (Rel. 38, last annotation update)
 CC DE ETS-DOMAIN PROTEIN EKL-1.
 CC GN EKL1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TAXID=10090;
 CC [1] SEQUENCE FROM N.A.
 CC RQ STRAIN=C7BL, TISSUE=Embryo;
 CC MEDLINE=97017146; PubMed=88033747;
 CC RA Grevin D., Ung S., Denhem F., Denhem M., Quatannens B., Begue A.,
 CC Stehelin D., Martin P.;
 CC "Structure and organization of the mouse ekl1 gene.";
 CC Gene 174:185-188(1996).
 CC [2] SEQUENCE OF 5'-224 FROM N.A.
 CC RC TISSUE=Embryo;
 CC RX MEDLINE=95047310; PubMed=7956835;
 CC RA Giovane A., Pintzas A., Maira S.-M., Sobieszczuk P., Wasyluk B.;
 CC "Net, a new ets transcription factor that is activated by Ras.";
 CC
 CC RL Genes Dev. 8:1502-1513(1994).
 CC -!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).
 CC
 CC DR EMBL; X87257; CAAG60715; 1; -.
 CC DR HSSP; P26939; CAR85391; 1; -.
 CC DR MIM: 310833; Etk1.
 CC DR InterPro: IPR000418; -.
 CC DR Pfam: PF00178; Ets; 1.
 CC DR PRINTS; PRO00454; ETS_DOMAIN.
 CC DR PROSITE; PS00345; ETS_DOMAIN; 1; 1.
 CC DR PROSITE; PS00346; ETS_DOMAIN; 2; 1.
 CC DR PROSITE; PS50031; ETS_DOMAIN; 3; 1.
 CC KW transcription regulation; Activator; Nuclear protein; DNA-binding;
 CC DNA_BIND 5 86 ETS DOMAIN.
 CC FT CONFLICT 133 133 P -> T (IN REF. 2).
 CC SEQUENCE 429 AA; 45243 MW; B61B9B97731D54F CRC64;
 CC
 CC Query Match 3.8%; Score 8; DB 1; Length 429;
 CC Best Local Similarity 100.0%; Pred. No. 1.1;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 189 PQKGKPR 196
 Db 311 PQKGKPR 318
 CC
 CC RESULT 3
 CC RL2_LEPIN STANDARD; PRT; 110 AA.
 CC ID RL2_LEPIN
 CC AC 09X031;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE 50S RIBOSOMAL PROTEIN L22.
 CC GN RP1V.
 CC OS Leptospira interrogans.
 CC OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
 CC OX NCBI_TAXID=173;
 CC RN [1] SEQUENCE FROM N.A.
 CC RP SPROTNE FROM N.A.
 CC RC STRAIN=SEROVAR Lai;
 CC RA Zuercher R.L., Hartskeerl R.A., van de Kamp H., Bal A.E.;
 CC RT Characterization of the Leptospira interrogans S10-spc-alpha
 CC operon. " Characterization of the Leptospira interrogans S10-spc-alpha
 CC RL FEMS Microbiol. Lett. 182:303-308(2000).
 CC CC -!- FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S RNA; ITS BINDING
 CC IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND L20.
 CC IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION
 CC CC IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION
 CC -!- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

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OM protein - protein search, using sw model
Run on: November 9, 2001, 15:34:35 ; search time 89.8 Seconds

(without alignments)
313.819 Million cell updates/sec

Title: US-09-668-021-2

Perfect score: 213

Sequence: 1 MOLFALALCILCLVHAFRV... KPRPRARSAKANGAELENAY 213

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Scanned: 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : SPTRIMBL_16:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_inhc:*

8: sp_lorcanelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	3.8	198	10 Q9FYQ3
2	8	3.8	276	13 Q9YGD6
3	8	3.8	276	13 Q9PT38
4	8	3.8	276	13 Q9PT37
5	8	3.8	276	13 Q9PT36
6	7	3.3	89	10 Q9FHT5
7	7	3.3	109	5 Q9GTJ4
8	7	3.3	114	5 Q9Q9K3
9	7	3.3	130	2 Q910C0
10	7	3.3	148	2 Q9IVX4
11	7	3.3	183	7 Q31243
12	7	3.3	186	10 Q9SDR7
13	7	3.3	197	2 Q9IYB9
14	7	3.3	197	2 Q9IYB9
15	7	3.3	251	2 Q911N0
16	7	3.3	282	10 Q9XF19
17	7	3.3	312	2 Q9RT99
18	7	3.3	321	2 Q9P972
19	3.3		398	1 Q00388

8

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PGGEAPRA 156

Db 83 PGGEAPRA 90

RESULT	1	PRELIMINARY;	PRT;	198 AA.
ID	Q9FYQ3			
AC	Q9FYQ3;			
DT	01-MAR-2001 (TREMBLrel. 16. Last sequence update)			
DT	01-MAR-2001 (TREMBL. 16. Last annotation update)			
DE	HYPOTHETICAL PROTEIN.			
OS	Oryza sativa (Rice)			
OC	Eukaryote; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
OC	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	Sasaki T., Matsumoto T., Yamamoto K.;			
RT	"Oriza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC clone: p0433fb05.\"",			
RT	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AP002539; BAB08182.1; SEQUENCE 198 AA; 21843 MW; 11DID90FE4B7F4E CRC64;			
DR	SEQUENCE 198 AA; 21843 MW; 11DID90FE4B7F4E CRC64;			
Query	Match	3.8%; Score 8; DB 10; Length 198:		
Best Local Similarity	100.0%; Pred. No. 2.7;			
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	149 PGGEAPRA 156			
Db	83 PGGEAPRA 90			
RESULT	2			
ID	Q9YGD6			
AC	Q9YGD6;			
PRT;	PRELIMINARY;			
PRT;	276 AA.			

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OM protein - protein search, using sw model

Run on : November 9, 2001, 15:30:31 ; Search time 47.66 Seconds
(without alignments)
100.571 Million cell updates/sec

title: US-09-668-021-2
perfect score: 213
Sequence: 1 MOLPLALICLVCLVHAFRV KPRPRARSAKANOAELENAY 213

Scoring table: OLIGO
Gapp 60.0 , Gapext 60.0

Search size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata2/1aa/5A, COMB.pep:*,
2: /cgn2_6/ptodata2/1aa/5B, COMB.pep:*,
3: /cgn2_6/ptodata2/1aa/6A, COMB.pep:*,
4: /cgn2_6/ptodata2/1aa/6B, COMB.pep:*,
5: /cgn2_6/ptodata2/1aa/pctus_comB.pep:*,
6: /cgn2_6/ptodata2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	4.2	206	1	US-08-468-847B-2
2	9	4.2	206	1	US-08-468-847B-20
3	9	4.2	206	4	US-09-188-930-159
4	9	4.2	206	4	US-09-188-930-286
5	7	3.3	114	1	US-08-582-257-15
6	7	3.3	114	2	US-08-582-257-15
7	7	3.3	186	4	US-09-4-75-316A-13
8	7	3.3	412	1	US-08-208-007A-12
9	7	3.3	412	4	US-08-974-631-4
10	7	3.3	917	2	US-08-588-933-16
11	7	3.3	917	2	US-08-588-976-16
12	6	2.8	39	3	US-08-554-305-22
13	6	2.8	68	2	US-08-836-791-5
14	6	2.8	80	1	US-08-011-308B-15
15	6	2.8	80	1	US-08-464-031-15
16	6	2.8	80	2	US-08-462-428-15
17	6	2.8	80	3	US-08-554-305-14
18	6	2.8	88	2	US-08-630-001A-31
19	6	2.8	97	2	US-08-245-511-30
20	6	2.8	97	2	US-08-600-933A-30
21	6	2.8	125	1	US-08-225-989-20
22	6	2.8	125	1	US-08-570-933-20
23	6	2.8	125	1	US-08-580-014-20
24	6	2.8	125	4	US-09-079-785-20
25	6	2.8	163	1	US-09-354-129-12
26	6	2.8	186	1	US-07-960-981-5
27	6	2.8	186	5	US-09-668-021-2

RESULTS

1

US-08-468-847B-2

Sequence 2, Application US/08468847B

Patent No. 5780263

GENERAL INFORMATION:

APPLICANT: Hastings, Gregg A. and Adams, Mark D.

TITLE OF INVENTION: Human CCN-Like Growth Factor

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468, 847B
FILING DATE: 6 June 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33, 073
REFERENCE/DOCKET NUMBER: 325800-442

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 205 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-468-847B-2

Query Match ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 Best Local Similarity 100.0%; Score 9; DB 1; Length 206;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188-930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 159
 LENGTH: 206
 TYPE: PRT
 ORGANISM: mouse
 US-09-188-930-159

RESULT 2
 US-08-468-847B-20
 ; Sequence 20 Application US/08468847B
 ; Patent No. 578023
 ; GENERAL INFORMATION:
 ; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 ; TITLE OF INVENTION: Human CCN-Like Growth Factor
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,847B
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; REFERENCE/DOCKET NUMBER: 325800-442
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCING CHARACTERISTICS:
 ; LENGTH: 206 AMINO ACIDS
 ; TYPE: AMINO ACID
 ; STRANDEDNESS:
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: PROTEIN
 ; US-08-468-847B-20

Query Match ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 Best Local Similarity 100.0%; Score 9; DB 4; Length 206;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188-930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206
 TYPE: PRT
 ORGANISM: mouse
 US-09-188-930-286

RESULT 4
 US-09-188-930-286
 ; Sequence 286 Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; TITLE OF INVENTION: and Methods For Their Use
 ; FILE REFERENCE: 11000.1011c1
 ; CURRENT APPLICATION NUMBER: US/09/188-930A
 ; CURRENT FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 348
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 286
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-188-930-286

Query Match ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 Best Local Similarity 100.0%; Score 9; DB 4; Length 206;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188-930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206
 TYPE: PRT
 ORGANISM: mouse
 US-09-188-930-286

RESULT 5
 US-08-582-257-15
 ; Sequence 15 Application US/08582257
 ; Patent No. 5763400
 ; GENERAL INFORMATION:
 ; APPLICANT: Adams, Michael E.
 ; APPLICANT: Zitran, Dusan
 ; TITLE OF INVENTION: Ecdysis-Triggering Hormone Compositions
 ; TITLE OF INVENTION: and Method for Use as Insecticides
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
 ; STREET: 816 Congress Avenue, Suite 1900
 ; CITY: Austin
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 78701

Query Match ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 Best Local Similarity 100.0%; Score 9; DB 1; Length 206;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188-930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 159
 LENGTH: 206
 TYPE: PRT
 ORGANISM: mouse
 US-09-188-930-159

RESULT 3
 US-09-188-930-159
 ; Sequence 159 Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James Greg

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5				
Run on:	November 9, 2001, 15:36:25 ; Search time 54.37 Seconds (without alignments) 298.422 Million cell updates/sec				
OM protein - protein search, using sw model					
Title:	US-09-668-021-6				
Perfect score:	213				
Sequence:	1 MQLPLAICLICLVLVHTAFRV KPRPRPARSAKANQAELENAY 213				
Scoring table:	OLIGO				
Gapop	60.0 , Gapext 60.0				
Searched:	219241 seqs, 76174552 residues				
Word size :	0				
Total number of hits satisfying chosen parameters:	219241				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing: Listing first 50 summaries					
Database :	PIR:68;* 1: pir1;* 2: pir2;* 3: pir3;* 4: pir4;*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query	Match Length	DB ID	Description
1	8	3.8	428	1	TVHUEK transforming protein elk-1 - human
2	8	3.8	429	2	JCA965 elk1 protein - nou
3	3	3.3	130	2	C8305 hypothetical protein
4	7	3.3	148	2	C83091 hypothetical protein
5	7	3.3	197	2	G81057 hypothetical protein
6	7	3.3	197	2	A81819 hypothetical protein
7	7	3.3	305	2	S77397 yabc protein homolog
8	7	3.3	312	2	D75344 conserved hypothetical protein
9	7	3.3	321	2	B82892 conserved hypothetical protein
10	7	3.3	328	2	S72647 hypothetical protein
11	7	3.3	398	1	S24802 polyferredoxin 6x2
12	7	3.3	408	2	D70365 fimbrial assembly
13	7	3.3	412	1	KHHD cathepsin D (EC 3.4.24.1)
14	7	3.3	510	2	S62801 legumin 31 precursors
15	7	3.3	512	1	WMCVFM inclusion body mat
16	7	3.3	562	2	T05758 hypothetical protein
17	7	3.3	587	2	T16617 hypothetical protein
18	7	3.3	602	2	S47880 NADH dehydrogenase
19	7	3.3	632	1	VGVNSY surface glycoprotein
20	7	3.3	681	2	E82812 outer membrane hem
21	7	3.3	781	1	TVFDFD protein kinase Dra
22	7	3.3	917	1	S15885 hexokinase (EC 2.7.1.1)
23	7	3.3	946	2	T16397 hypothetical protein
24	7	3.3	1940	2	A59287 myosin heavy chain
25	7	3.3	6420	2	T30283 polyketide syntas
26	6	2.8	49	2	S29215 neurotoxin Tx2 - s
27	6	2.8	65	2	B25025 malX protein - Kie
28	6	2.8	72	2	T00523 hypothetical protein
29	6	2.8	83	2	S41672 tightly associated

Gene 174, 185-188, 1996
 A;Title: Structure and organization of the mouse elkl gene.
 A;Reference number: JG4965; MUID:97017146
 A;Accession: JG4965
 A;Molecule type: mRNA
 A;Residues: 1-129 <SRE>
 A;Cross-references: EMBL:X87257; NID:9836634; PIDN:CAA60715.1; PID:9836635
 A;Experimental source: embryo
 R;Giovane, A.; pintas, A.; Maira, S.M.; Sobieszczuk, P.; Wasyluk, B.
 Genes Dev. 8, 1502-1513, 1994
 A;Title: Net, a new ets transcription factor that is activated by Ras.
 A;Reference number: A53837; MUID:9504710
 A;Accession: I48339
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-129 <SRE>
 A;Cross-references: EMBL:X87257; NID:9836634; PIDN:CAA60715.1; PID:9836635
 A;Accession: I48340
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 5-132, 'T', 124-224 <RE2>
 C;Cross-references: EMBL:Z3639; NID:9535922; PIDN:CAA85391.1; PID:9535923
 C;Comment: This protein belongs to the subfamily of ternary complex factor (TCF) which includes the TCF-1, TCF-2, and TCF-3 proteins.
 C;Genetics:
 A;Gene: elkl
 A;Introns: 70/3; 219/3; 363/3; 397/3
 C;Superfamily: elk-1-transforming protein; ets DNA-binding domain homology <ETS>
 F;7-86/Domain: ets DNA-binding domain homology <ETS>

Query Match 3.8%; Score 8; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 189 PQKGRKPR 196
 |||||||
 Db 311 PQKGRKPR 318

RESULT 3
 DB3305 hypothetical protein PA2722 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
 C;Accession: DB3305
 R;Stover, C.K.; Pham, X.Q.; Elwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:2043737
 A;Accession: DB3305
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-130 <STO>
 A;Cross-references: GB:AE004700; GB:AE004091; NID:99948792; PIDN:AG06110.1; GSPDB:GN001
 A;Experimental source: Strain PA01
 C;Genetics:
 A;Gene: PA2722

Query Match 3.3%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 158 KVRLVAS 164
 |||||||
 Db 12 KVRLVAS 18

RESULT 4
 C83091 hypothetical protein PA4441 [imported] - Pseudomonas aeruginosa (strain PA01)

Query Match 3.3%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 203 KANQAEI 209
 |||||||
 Db 122 KANQAEI 128

RESULT 6
 A81819 hypothetical protein NMA1913 [imported] - Neisseria meningitidis (strain 22491 serogroup A)
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: A81819
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Moore, D.; Holroyd, S.; Jagger, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755
 A;Accession: G81057
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-197 <TET>
 A;Cross-references: GB:AE002516; GB:AE002098; NID:9726905; PIDN:AAF42005.1; PID:97224000
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1656

Query Match 3.3%; Score 7; DB 2; Length 197;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 203 KANQAEI 209
 |||||||
 Db 122 KANQAEI 128

RESULT 6
 A81819 hypothetical protein NMA1913 [imported] - Neisseria meningitidis (strain 22491 serogroup A)
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: A81819
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Moore, D.; Holroyd, S.; Jagger, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
 A;Reference number: A81775; MUID:2022556
 A;Accession: A81819
 A;Status: preliminary

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5		
OM protein - protein search, using sw model			
Run on:	November 9, 2001, 15:47:54 ; Search time 31.03 seconds		
Perfect score:	US-09-668-021-6		
Sequence:	1 MOLPLAICLICLIVHTAERV. KFRPRARSAKANQABLENAY 213		
Scoring table:	OLIGO		
Word size :	0		
Searches:	93435 seqs, 34255486 residues		
Total number of hits satisfying chosen parameters:	93435		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Listing first 50 summaries		
Database :	SwissProt_39;*		
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
Result No.	Query Length	DB ID	Description
1	8	3..8	428 1 ELKL_HUMAN
2	8	3..8	429 1 ELKL_MOUSE
3	7	3..3	110 1 RL22_LPRIN
4	7	3..3	305 1 YB44_STHN3
5	7	3..3	412 1 CAND_HUMAN
6	7	3..3	512 1 IBMP_FMDA
7	7	3..3	602 1 NUTM2_DIDMA
8	7	3..3	632 1 VGLG_SYN
9	7	3..3	781 1 KRAF_DROME
10	7	3..3	917 1 HKX2_MOUSE
11	7	3..3	917 1 HKX2_RAT
12	6	2..8	49 1 TX25_PHONE
13	6	2..8	65 1 MAIX_KLREP
14	6	2..8	97 1 OSPC_CHICK
15	6	2..8	97 1 VET2 HPV4
16	6	2..8	110 1 RL22_ECOLI
17	6	2..8	111 1 RL22_ACHILIA
18	6	2..8	112 1 RL22_SPIDI
19	6	2..8	113 1 RL22_THRTH
20	6	2..8	115 1 TIAF_HUMAN
21	6	2..8	115 1 TIAF_MOUSE
22	6	2..8	118 1 REV_HVILW
23	6	2..8	123 1 RS12_ECOLI
24	6	2..8	131 1 RL22_PHYS1
25	6	2..8	167 1 BMR_MEUR
26	6	2..8	168 1 TRIC_CHECK
27	6	2..8	175 1 R16A_YEST
28	6	2..8	182 1 YCVO_YEAR
29	6	2..8	196 1 REB2_CHICK
30	6	2..8	206 1 BTP3_HUMAN
31	6	2..8	210 1 TREP_KLULIA
32	6	2..8	211 1 YR73_MEWR
33	6	2..8	213 1 PYRE_HABIN
SUMMARIES			
RESULTS			
RESULT 1	ELKL_HUMAN		
ELKL_HUMAN	STANDARD; PRT; 428 AA.		
ID	P19419; 075606; Q9UJ4; 095058;		
AC	P19419; 075606; Q9UJ4; 095058;		
RA	Reedy E.S.P.;		
RT	translocation-specific ets-related genes on chromosomes X and 14 near		
RL	Science 244:66-70(1999).		
RN	[2]		
RE	elk1, tissue-specific ets-related genes on chromosomes X and 14 near		
RP	translocation-specific breakpoints.;		
RT	Science 244:66-70(1999).		
RN	[2]		
RE	SEQUENCE FROM N.A.		
RP	MEDLINE=9903876; PubMed=9795224;		
RA	Hazrindranath N., Mills F.C., Mitchell M.P., Meindl A., Max E.F.;		
RT	"The human elk-1 gene family: the functional gene and two processed		
RP	pseudogenes embedded in the IgH locus.;"		
RA	Gene 221:215-224(1998).		
RN	[3]		
RE	SEQUENCE FROM N.A.		
RA	Graham D.;		
RT	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RE	SEQUENCE FROM N.A. (ISOFORM 2).		
RA	Artee D.N.T., Kovar H.,		
RT	"Novel family members HuER71, ELF8, and ELKV among ETS-related genes		
RT	coexpressed with EWS-FLI1 in Ewing tumor cell lines;"		
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RE	DOMAINS.		
RA	MEDLINE=92334979; PubMed=1630903;		
RT	Jenknecht R., Nordheim A.;		
RT	"ELK-1 protein Domains required for direct and SRF-assisted		
RT	DNA-binding;"		
RL	Nucleic Acids Res. 20:3317-3344(1992).		
CC	-I- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA		
CC	SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE		
CC	FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE		
CC	ELEMENT		
CC	-I- SUBCELLULAR LOCATION: NUCLEAR.		
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE		

CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: LUNG AND TESTIS.
 CC -!- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
 CC AND ERK).
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; M25269; AAA52384.1; -.
 CC DR EMBL; AF000672; AAC00862.1; -.
 CC DR EMBL; AF009172; CA15659.1; -.
 CC DR EMBL; AF000672; AAC00862.1; -.
 CC DR EMBL; AF11354; TVHUEK.
 CC DR HSSP; P11921; 2STW.
 CC DR TRANSFAC; T00250; -.
 CC DR MIM; 311040; -.
 CC DR InterPro; IPR000418; -.
 CC DR Pfam; PF00178; Ets: 1.
 CC DR PRINTS; PRO0454; ETS_DOMAIN.
 CC DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 CC DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 CC DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
 CC KW transcription regulation; Activator; Nuclear protein; DNA-binding;
 CC Phosphorylation; Alternative splicing;
 CC DNA_BIND 5 86
 CC FT VARSPLIC 91 95
 CC FT VARSPLIC 96 428
 CC DE CONFFLICT 183 183
 CC SQ SEQUENCE 428 AA; 44888 MN; 68F71F8AD9D38CA CRC64;
 CC -----
 CC Query Match 3.8%; Score 8; DB 1; Length 428;
 CC Best Local Similarity 100.0%; Pred. No. 1.1;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 OY 189 POKGRKPR 196
 CC DB 310 POKGRKPR 317
 CC -----
 CC RESULT 2
 CC ERL1_MOUSE STANDARD: PRT: 429 AA.
 CC ID_ERL1_MOUSE P41959; 01-NOV-1995 (Rel. 32, created)
 CC DT 01-OCT-1996 (Rel. 34, last sequence update)
 CC DT 15-JUL-1999 (Rel. 38, last annotation update)
 CC DE ETS-DOMAIN PROTEIN ERL1.
 CC GN ERL1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 CC OR NCBI_TaxID=10090;
 CC RN SEQUENCE FROM N.A.
 CC RC STRAIN=C57BL/6; TISSUE=Embryo; MEDLINE=9701746; PubMed=8803747;
 CC RX Grevin D., Ugg S., Denhez F., Dehenn M., Quatannens B., Begue A.,
 CC RA Stehelin D., Martin P.; Structure and organization of the mouse elkl gene.;
 CC RT Gene 174:185-188(1996).
 CC RN [1] SEQUENCE OF 5-224 FROM N.A.
 CC RC TISSUE=Embryo; MEDLINE=9047310; PubMed=7958835;
 CC RA Giovane A., Pintzas A., Maia S.-M., Sobieszcak P., Wasyluk B.; Net, a new ets transcription factor that is activated by Ras.;
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 CC -----
 CC DR EMBL; X87257; CAA60715.1; -.
 CC DR EMBL; Z36939; CAB85391.1; -.
 CC DR HSSP; P14921; 2STW.
 CC DR MGD; MGI:01833; ERL1.
 CC DR InterPro; IPR000418; -.
 CC DR Pfam; PF00178; Ets: 1.
 CC DR PRINTS; PRO0454; ETS_DOMAIN.
 CC DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 CC DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 CC DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
 CC KW transcription regulation; Activator; Nuclear protein; DNA-binding;
 CC Phosphorylation;
 CC DNA_BIND 5 86
 CC FT CONFFLICT 133 133
 CC SQ SEQUENCE 429 AA; 45243 MN; B61B5977731DS4F_CRC64;
 CC -----
 CC Query Match 3.8%; Score 8; DB 1; Length 429;
 CC Best Local Similarity 100.0%; Pred. No. 1.1;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 OY 189 POKGRKPR 196
 CC DB 311 POKGRKPR 318
 CC -----
 CC RESULT 3
 CC ID_RL22_LEPIN ID_RL22_LEPIN STANDARD: PRT: 110 AA.
 CC AC Q9XD31; DT 30-MAY-2000 (Rel. 39, created)
 CC DT 30-MAY-2000 (Rel. 39, last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, last annotation update)
 CC DE 50S RIBOSOMAL PROTEIN L22.
 CC GN RPLV.
 CC OS Leptospira interrogans.
 CC OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
 CC OX NCBI_TaxID=173;
 CC RN [1] SEQUENCE FROM N.A.
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=SEROVAR LAI; MEDLINE=20088135; PubMed=10620683;
 CC RA Zuercher R.L., Harmskeer R.A., van de Kemp H., Bai A.E.;
 CC RT Characterization of the Leptospira interrogans S10-spec-alpha
 CC RT operon.; RL FEMS Microbiol. Lett. 182:303-308 (2000).
 CC CC IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND L20.
 CC CC IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION
 CC CC (BY SIMILARITY).
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 CC -----
 RL Genes Dev. 8:1502-1513(1994).
 CC -!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -----
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A
 CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
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 CC -----
 RL Genes Dev. 8:1502-1513(1994).
 CC -!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -----
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A
 CC LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
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OM protein - protein search, using sw model

Run on: November 9, 2001, 15:47:17 ; Search time 89.8 Seconds
(without alignments)

313.819 Million cell updates/sec

Title: US-09-668-021-6

Perfect score: 213

Sequence: 1 MOLPLALCLICLVLVHTAFRV KPRPRARSAKANQAELENAY 213

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : SPTREMBL16:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	3.8	198	10 Q9FYQ3
2	8	3.8	276	13 Q9YGD6
3	8	3.8	276	13 Q9PT39
4	8	3.8	276	13 Q9PT37
5	8	3.8	276	13 Q9PT36
6	8	3.8	1064	4 Q9NQ38
7	8	3.8	1064	4 Q9NQ38
8	7	3.3	89	10 Q9FH55
9	7	3.3	109	5 Q9GTJ4
10	7	3.3	130	2 Q91OC0
11	7	3.3	148	7 Q9HVX4
12	7	3.3	186	10 Q9SDR7
13	7	3.3	197	2 Q9JYB9
14	7	3.3	197	2 Q9JTA0
15	7	3.3	208	2 Q95M81
16	7	3.3	251	10 Q9L1N0
17	7	3.3	282	10 Q9XFI9
18	7	3.3	312	2 Q9RT99
19	7	3.3	321	2 Q9PQ72

ALIGNMENTS

RESULT 1

Q9FYQ3 PRELIMINARY; PRT; 198 AA.

ID Q9FYQ3; AC Q9FYQ3; DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update) DE HYPOTHETICAL PROTEIN.

OS Oryza sativa (Rice).
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhardtioideae; Oryzeae; OC Oryza.
OC NCBI_TaxID:4530; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV_NIPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;
'Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC

RT clone P0433F09; ";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AP002539; BAB08182.1; -.

SQ SEQUENCE 198 AA; 21843 MW; 11D1D90FE4B72F4E CRC64;

Query Match Best Local Similarity 100.0%; Score 8; DB 10; Length 198; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PGEAAPPRA 156

Db 83 PGEAAPPRA 90

RESULT 2

ID Q9YGD6 PRELIMINARY; PRT; 276 AA.

AC Q9YGD6;

Query Match 3 8%; Score 8; DB 13; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.3; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Qy 28 AFKNDATE 35
 Db 93 AFKNDATE 100

RESULT 4
 Q9PT37 PRELIMINARY; PRT; 276 AA.

ID Q9PT37
 AC Q9PT37;
 DT 01-MAY-2000 (TREMBLel. 13, Created)
 DT 01-MAY-2000 (TREMBLel. 13, Last sequence update)

DE CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

[1] SEQUENCE FROM N.A.

RN

RX MEDLINE=99185307; PubMed=10082666;

RA Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

RT "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";

RT Blochim. Biophys. Res. Commun. 255:123-128(1999).

-1 SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

DR EMBL: AF100930; AAD20217.1; -.

DR HSSP: P50163; ZAE1.

DR InterPro: IPR002198; -.

DR InterPro: IPR002347; -.

DR Pfam: PF00106; adh.short; 1.

DR PRINTS: PR00080; SDRFAMILY.

KW Oxidoreductase.

SEQUENCE 276 AA; 30111 MW; 135604A38D2940CD CRC64;

Query Match 3 8%; Score 8; DB 13; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.3; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Qy 28 AFKNDATE 35
 Db 93 AFKNDATE 100

RESULT 3
 Q9PT38 PRELIMINARY; PRT; 276 AA.

ID Q9PT38
 AC Q9PT38;
 DT 01-MAY-2000 (TREMBLel. 13, Created)
 DT 01-MAY-2000 (TREMBLel. 13, Last sequence update)

DE CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE A.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

[1] SEQUENCE FROM N.A.

RN

RX MEDLINE=99185307; PubMed=10082666;

RA Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

RT "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";

RT Blochim. Biophys. Res. Commun. 255:123-128(1999).

-1 SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

DR EMBL: AF100932; AAD20991.1; -.

DR HSSP: P50163; ZAE1.

DR InterPro: IPR002198; -.

DR InterPro: IPR002347; -.

DR Pfam: PF00106; adh.short; 1.

DR PRINTS: PR00081; SDRFAMILY.

KW Oxidoreductase.

SEQUENCE 276 AA; 30127 MW; 1350E4211D34225D CRC64;

Query Match 3 8%; Score 8; DB 13; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.3; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RT

Qy 28 AFKNDATE 35
 Db 93 AFKNDATE 100

RESULT 5
 Q9PT36 PRELIMINARY; PRT; 276 AA.

ID Q9PT36
 AC Q9PT36;
 DT 01-MAY-2000 (TREMBLel. 13, Created)
 DT 01-MAY-2000 (TREMBLel. 13, Last sequence update)

DE CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE A.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

[1] SEQUENCE FROM N.A.

RN

RX MEDLINE=99185307; PubMed=10082666;

RA Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

RT "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";

RT Blochim. Biophys. Res. Commun. 255:123-128(1999).

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Run on: November 9, 2001, 15:34:28 ; Search time 79.75 Seconds
(without alignments)

18.91 / Million cell updates/sec

Perfect score: 213
Sequence: I MQLPLALLCLICLICLVHTAERV KPRRARSAKANOAELENAY 213

Scoring table.
Oligo 60.0, Gapop 60.0, Gapext 60.0

ord size : 0

Minimum DB seq length: 0

Post-processing: Listing first 50

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butunca :  
1: /SIDS8/gcadata/geneseq/geneseqp/AA1980.DAT: *  
2: /SIDS8/gcadata/geneseq/geneseqp/AA1981.DAT: *
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4: /SIDS8/gcgdat  
5: /SIDS8/gcgdat  
6: /SIDS8/gcgdat
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7:
8: /SIDS8/gcgdata
9: /SIDS8/gcgdata

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11: /SIDS8/gcgda  
12: /SIDS8/gcgda  
13: /SIDS8/gcgda
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14: /SIDS8/gcggda
15: /SIDS8/gcggda
16: /SIDS8/gcggda

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18: /$IDS8/gcgda  
19: /$IDS8/gcgda  
20: /$IDS8/gcgda
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21: /SIDS8/gcqda
22: /SIDS8/gcqda

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	213	100.0	213	21	AYY96430	Human TGF-beta bin
2	203	95.3	213	21	AYY96436	Human TGF-beta bin
3	175	82.2	213	21	AYB26106	Human DAN/Cerberus
4	175	82.2	213	21	AYY96429	Human TGF-beta bin
5	175	82.2	213	22	AYY97589	Human secreted pro
6	139	65.3	367	21	AYB26105	Human DAN/Cerberus
7	113	53.3	213	21	AYY96431	Vervet TGF-beta bin
8	76	35.7	176	21	AYY96434	Bovine TGF-beta bin
9	33	15.5	213	21	AYY96433	Rat TGF-beta bindi
10	32	15.0	211	21	AYY96432	Murine TGF-beta bin
11	27	12.7	50	20	AYY12009	Human 5' EST secre

Multine IGF Beta B1 Human 5' EST secre

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

ZIMMERMANN

XX	PA	FT	Misc-difference 38
XX	XX	FT	/label= P38R
PI	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;	FT	/note= "wild type" proline has been substituted with
PI	Van Ness J, Winkler DG;	FT	arginine
XX	DR	XX	WPI; 2000-412321/35.
XX	DR	XX	N-PSDB; AAA29056.
PT	Nucleic acids (1) encoding a transforming growth factor beta binding	PR	protein, useful for identifying agents for treating osteopenia,
PT	osteoporosis and fractures	PS	Claim 3; Page 119-120; 162PP; English.
XX	CC	XX	This shows a variant human transforming growth factor-beta (TGF-beta) binding protein designated BEER VII, which comprises a substitution of isoleucine for the wild-type valine at residue 10. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression.
CC	CC	XX	The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
CC	CC	XX	Sequence 213 AA;
Query Match	100.0%; Score 213; DB 21; Length 213;		
Best Local Similarity	100.0%; Pred. No. 4.5e-214;		
Matches	213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MQLPLAICLCLLVLVIAFRVVEGQWQAFRNDATEILRELGEYPEPPPELENKTMNRAE 60		
Db	1 mqiplaiclcllvtarfveggwqafndateilrelgeypepppelemtmrae 60		
QY	61 NGGRPPPHPPFETKDVSEYSCRELHTRYDGRPSAKPTVTELVCSQCGPARLLPNAG 120		
Db	61 ngrgrphphpfetkdvseycrelhtrydgrpsakptvtelvsgqcgparllpnag 120		
QY	121 RGKWWRPPSGDFRCIPDRYRQARQVOLCPCGGEARPARKVRLAVSCKKRLTRFHNQSELK 180		
Db	121 rggkwrrppsgdfrcipdrypyraqvqlcpcggearparkvrlavscckrltrfhnqselk 180		
QY	181 DFGTEARPKGRKRPRPARSAKANQALEENAY 213		
Db	181 dfgtearpkgrkrprparsakanaqelenay 213		
Query Match	95.3%; Score 203; DB 21; Length 213;		
Best Local Similarity	100.0%; Pred. No. 1.2e-203;		
Matches	203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	11 CLVHTARRVVEQGQWQAFRNDATEILRELGEYPEPPPELENKTMNRAEENGRRPHPF 70		
Db	11 clvhhtarrveggwqafndateilrelgeypepppelemtmraengrrphpf 70		
QY	71 ETKDVSEYSCRELHTRYVTGCRSAKPVTELVCSQCGPARLLPNAIGRKWWRPSGP 130		
Db	71 etkdvseycrelhtryvtgpcrsakpvtevcsgqcgparllpnraigrkwwrpsgp 130		
QY	131 DFRCPDPRYDRAORVOLCPCGGEARPARKVRLAVSCKKRLTRFHNQSELKDFGTARPO 190		
Db	131 dfrcpdprydraqvqlcpcggearparkvrlavscckrltrfhnqselkdfgtarpo 190		
QY	191 KGKPRPRPARSAKANQALEENAY 213		
Db	191 kgkprprparsakanaqelenay 213		
RESULT	2		
AY96436	AY96436 standard; Protein; 213 AA.		
XX	AY96436;		
XX	12-SEPP-2000 (first entry)		
DE	Human TGF-beta binding protein (BEER) variant P38R.		
XX	KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein; variant; P38R; gene therapy; antisense therapy; fracture; KW chromosome 17q12-21; bone mineralization.		
OS	XO Homo sapiens.		
XX	Key		Location/Qualifiers

GenCore version 4.5
copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:35:22 ; Search time 47.66 Seconds
(without alignments)
100.571 Million cell updates/sec

Title: US-09-668-021-6
Perfect score: 213
Sequence: 1 MQLPLAICLICLVLHTAFRV. KPRPRARSAKANQALENAY 213

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_AA:*

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3: /ccn2_6/ptodata/2/iaa/6A_COMB_pep:*

4: /ccn2_6/ptodata/2/iaa/6B_COMB_pep:*

5: /ccn2_6/ptodata/2/iaa/PCNTS_COMB_pep:*

6: /ccn2_6/ptodata/2/iaa/Backfilest1_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-09-468-847B-2
; Sequence 2, Application US/08468847B
; Patent No. 5780263
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNIE, BAIN, GILFILIAN,
; ADDRESSEER: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; ZIP: 07068
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; STEREOCHEMISTRY:
; TOPOGONY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-468-847B-2

Sequence 2, Appli
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Best Local Similarity 100.0%;  Pred. No. 0.29;  Length 206;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   28 AFKNDATEI 36
Db   23 AFKNDATEI 31

RESULT 2
US-08-468-847B-20
Sequence 20, Application US/08468847B
PATENT NO. 5780263
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CECCHI, STUART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847B
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-468-847B-20

Query Match        4.2%;  Score 9;  DB 1;  Length 206;
Best Local Similarity 100.0%;  Pred. No. 0.29;  Length 206;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   28 AFKNDATEI 36
Db   23 AFKNDATEI 31

RESULT 3
US-09-188-930-159
Sequence 159, Application US/09188930A
PATENT NO. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
and Methods For Their Use
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 286
LENGTH: 206
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-286

Query Match        4.2%;  Score 9;  DB 4;  Length 206;
Best Local Similarity 100.0%;  Pred. No. 0.29;  Length 206;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   28 AFKNDATEI 36
Db   23 AFKNDATEI 31

RESULT 4
US-09-188-930-286
Sequence 286, Application US/09188930A
PATENT NO. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
and Methods For Their Use
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 286
LENGTH: 206
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-286

Query Match        4.2%;  Score 9;  DB 4;  Length 206;
Best Local Similarity 100.0%;  Pred. No. 0.29;  Length 206;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy   28 AFKNDATEI 36
Db   23 AFKNDATEI 31

RESULT 5
US-09-475-316A-13
Sequence 13, Application US/09475316A
PATENT NO. 6210942
GENERAL INFORMATION:
APPLICANT: Lewis, No. 6210942man G.
APPLICANT: Davin, Laurence B.
APPLICANT: Drinkova-Kostova, Albena T.
APPLICANT: Fujita, Masayuki
APPLICANT: Gang, David R.
APPLICANT: Saksanen, Simo
APPLICANT: Ford, Joshua D.
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, Greg
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES
TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
FILE REFERENCE: W09-1-1373
CURRENT APPLICATION NUMBER: US/09/475,316A
CURRENT FILING DATE: 1999-12-30

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On protein - protein search, using sw model	GenCore version 4.5	30	7	3.3	962	2	A81817
Copyright (c) 1993 - 2000 Compugen Ltd.		31	7	3.3	962	2	C81060
Run on:	November 9, 2001, 15:36:26 ; Search time 54.37 Seconds	32	7	3.3	1168	1	MWAXIC
Scoring table:	OLIGO	33	7	3.3	1308	2	T15280
Word size :	219241 seqs, 76174552 residues	34	7	3.3	1940	2	A59287
Total number of hits satisfying chosen parameters:	219241	35	7	3.3	6420	2	T30283
Minimum DB seq length: 0		36	6	2.8	22	2	JP0066
Maximum DB seq length: 200000000		37	6	2.8	49	2	S29215
Post-processing: Listing first 50 summaries		38	6	2.8	65	2	B25025
Database :	PIR_68;*	39	6	2.8	83	2	S41672
	1: pir1;*	40	6	2.8	89	2	D75271
	2: pir2;*	41	6	2.8	101	2	I57492
	3: pir3;*	42	6	2.8	102	2	G85584
	4: pir4;*	43	6	2.8	102	2	T51524
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		45	6	2.8	108	2	T49144
		46	6	2.8	110	1	R5EC22
		47	6	2.8	110	1	H8596
		48	6	2.8	111	2	C41839
		49	6	2.8	113	2	S66512
		50	6	2.8	118	2	T05520
Total number of hits satisfying chosen parameters:	219241						ALIGNMENTS
Minimum DB seq length: 0							
Maximum DB seq length: 200000000							
Post-processing: Listing first 50 summaries							
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	2: pir2;*						
	3: pir3;*						
	4: pir4;*						
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
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					TVHUEK		
1	8	3.8	428	1	transforming protein elk-1 - human		
2	8	3.8	429	2	elk1 protein - mouse	C;Species: Homo sapiens (man)	
3	8	3.8	850	2	Erbb kinase actina	C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999	
4	7	3.3	99	1	beta-2-microglobul	C;Accession: A41354; SS4721	
5	7	3.3	119	2	transcription acti	R;Rao, V.N.; Rheeber, K.; Isobe, M.; ar-Rushdi, A.; Croce, C.M.; Reddy, E.S.P.	
6	7	3.3	130	2	hypothetical prote	A;Title: elk1, tissue-specific ets-related genes on chromosomes x and 14 near transloc	
7	7	3.3	148	2	transforming prote	A;Reference number: A41354; MUID:95196758	
8	7	3.3	183	2	elk1 protein - mou	A;Molecule type: mRNA	
9	7	3.3	197	2	Erbb kinase actina	A;Residues: 1-428 <Rao>	
10	7	3.3	197	2	beta-2-microglobul	R;Gille, H.; Kortenmann, M.; Thomae, O.; Moomaw, C.; Slaughter, C.; Cobb, M.H.; Shaw, E.M.; Cross references: GB:M25269; NID:9538208; PIDN:AAA52384.1; PID:9538209	
11	7	3.3	230	2	transcription acti	A;Title: Elk phosphorylation potentiates Elk-1-mediated ternary complex formation and	
12	7	3.3	321	2	hypothetical prote	A;Reference number: S547471; MUID:95196758	
13	7	3.3	328	2	hypothetical prote	A;Accession: S547471	
14	7	3.3	398	1	hypothetical prote	A;Status: preliminary	
15	7	3.3	408	2	hypothetical prote	A;Molecule type: protein	
16	7	3.3	412	1	hypothetical prote	A;Residues: 318-328,'XX',331,336-364;380-388,'X',390-392,'X',394-400,'XX',403-405,'X'	
17	7	3.3	459	2	hypothetical prote	C;Genetics: C;Gene: GBB:ELK1	
18	7	3.3	461	2	hypothetical prote	A;Cross-references: GDB:119867; OMIM:311040	
19	7	3.3	510	2	hypothetical prote	A;Map position: Xp11.2-q11.2	
20	7	3.3	562	2	hypothetical prote	C;Superfamily: elk-1 transforming protein; ets DNA-binding domain homology	
21	7	3.3	573	2	hypothetical prote	C;Keywords: DNA binding; oncogene; transforming protein	
22	7	3.3	587	2	hypothetical prote	R:7-86(Domain: ets DNA-binding domain homology <ETSS>	
23	7	3.3	602	2	hypothetical prote		
24	7	3.3	632	1	hypothetical prote		
25	7	3.3	681	2	hypothetical prote		
26	7	3.3	829	2	hypothetical prote		
27	7	3.3	864	2	hypothetical prote		
28	7	3.3	900	2	hypothetical prote		
29	7	3.3	917	1	hypothetical prote		
					RESULT	2	
					JC4955		
					elk1 protein - mouse		
					C;Species: Mus musculus (house mouse)		
					C;Date: 31-Dec-1995 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999		
					C;Accession: JC4955; 148339; 148440; S54908		
					R;Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin, D.		

Gene 174, 185-188, 1996

A;Title: Structure and organization of the mouse elk1 gene.

A;Reference number: JG4965

A;Molecule type: mRNA

A;Residues: 1-429 <GRE>

A;Cross-references: EMBL:X87257; NID:9836634; PIDN:CA60715.1; PID:9836635

A;Experimental source: embryo

R;Giovane, A.; Pintzas, A.; Maira, S.M.; Sobieszcuk, P.; Wasyluk, B.

Genes Dev. 8, 1502-1513, 1994

A;Title: Net, a newets transcription factor that is activated by Ras.

A;Reference number: A53837; MUID:95047310

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-429 <REB>

A;Cross-references: EMBL:X87257; NID:9836634; PIDN:CA60715.1; PID:9836635

A;Molecule type: mRNA

A;Residues: 5-132; '1',134-224 <REB>

A;Cross-references: EMBL:Z46932; PIDN:CA85391.1; PID:9535923

A;Comment: This protein belongs to the subfamily of ternary complex factor (TCF) which t

C;Genetics:

A;Gene: elk1

A;Introns: 70/3; 219/3; 363/3; 397/3

C;Superfamily: elk-1 transforming protein; ets DNA-binding domain homology <ETS>

F;7-86/domain: ets DNA-binding domain homology

Query Match 3.88; Score 8; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 189 PQKGRKPR 196
 |||||||
 Db 311 PQKGRKPR 318

RESULT 3

JC5700

ERBB kinase activator alpha, brain and thymus - human

C;Species: Homo sapiens (man)

C;Date: 25-Nov-1997

C;Accession: JC5700

C;Comment: This protein is a member of the epidermal growth factor family. It is functional

C;Superfamily: unassigned EGF-related proteins; EGF homology

C;Keywords: glycoprotein

F;258-311/Domain: Ig-like #status predicted <IGL>

A;Title: A novel brain-derived member of the epidermal growth factor family that interacts

A;Reference number: JC5700; MUID:98006324

A;Accession: JC5700

A;Status: nucleic acid sequence not shown

A;Residues: 1-850 <HIG>

A;Cross-references: DBJ:AB00560; NID:92626738; PIDN:BAA23417.1; PID:92626739

A;Experimental source: SK-NH cell

C;Comment: This protein is a member of the epidermal growth factor family. It is functional

C;Superfamily: unassigned EGF-related proteins; EGF homology

F;258-311/Domain: Ig-like #status predicted <IGL>

F;346-381/Domain: EGF-like #status predicted <EGF>

F;147,278,451/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.88; Score 8; DB 2; Length 850;

A;Cross-references: DBJ:AB00560; NID:92626738; PIDN:BAA23417.1; PID:92626739

A;Experimental source: SK-NH cell

C;Comment: This protein is a member of the epidermal growth factor family. It is functional

C;Superfamily: unassigned EGF-related proteins; EGF homology

F;258-311/Domain: Ig-like #status predicted <IGL>

F;346-381/Domain: EGF-like #status predicted <EGF>

Query Match 3.88; Score 8; DB 2; Length 850;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 195 PPRARGA 202
 |||||||

Db 725 PPRARGA 732

RESULT 4

MGPB2

beta-2-microglobulin - guinea pig

N;Alternative names: class I histocompatibility antigen beta chain

C;Species: Cavia porcellus (guinea pig)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Jan-1997

C;Accession: A02181

R;Wolfe, P.B.; Cebray, J.J.

Mol. Immunol. 17, 1493-1505, 1980

A;Title: The primary structure of guinea pig beta2-microglobulin.

A;Reference number: A02181; MUID:82057805

A;Accession: A02181

A;Molecule type: Protein

A;Residues: 1-99 <WOL>

C;Function:

A;Description: necessary for the expression of MHC class I histocompatibility antigen

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: heterodimer

F;18-82/Domain: immunoglobulin homology <IMM>

F;25-80/Disulfide bonds: #status predicted

Query Match 3.3%; Score 7; DB 1; Length 99;

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 LLVHAAP 18
 |||||
 Db 64 LLVHAAP 70

RESULT 5

S4292

transcription activator - Emmericella nidulans

C;Species: Emmericella nidulans Aspergillus nidulans

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Jul-1998

C;Accession: S4292

R;Kulmburg, P.; Prange, T.; Mathieu, M.; Sequeval, D.; Scazzocchio, C.; Felenbok, B.

FEBS Lett. 280, 11-16, 1991

A;Title: Correct intron splicing generates a new type of a putative zinc-binding dom

A;Reference number: S4292; MUID:9184391

A;Accession: S4292

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-119 <KUL>

C;Superfamily: GAL4 zinc binuclear cluster homology <GAL4>

F;7-54/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 3.3%; Score 7; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 GAAPRAR 157
 |||||
 Db 63 GAAPRAR 69

RESULT 6

DB3305

hypothetical protein PA2722 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: DB3305

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;

admin, S.; yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A;Accession: DB3305

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:47:55 ; Search time 31.03 Seconds
(without alignments)

Maximum DB seq length: 0
Post-processing: Listing first 50 summaries

Scoring table: OLIGO
Database: SwissProt_39.*

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	8	3.8	428	1	EIRL_HUMAN
2	8	3.8	429	1	EIRL_MOUSE
3	8	3.8	850	1	NRG2_HUMAN
4	7	3.3	99	1	B2MG_CAVPO
5	7	3.3	110	1	R122_LFRPIN
6	7	3.3	230	1	CATD_HUMAN
7	7	3.3	412	1	IP3K_RAT
8	7	3.3	459	1	IP3K_HUMAN
9	7	3.3	361	1	NU5M_DIDMA
10	7	3.3	602	1	VGIG_SINV
11	7	3.3	632	1	AVCR_EMENI
12	7	3.3	821	1	IF2_HAEMIN
13	7	3.3	829	1	IF2_MCYCTU
14	7	3.3	900	1	HXR2_MOUSE
15	7	3.3	917	1	HXR2_RAT
16	7	3.3	924	1	IF2_MCYCLE
17	7	3.3	1168	1	MYSC_ACACA
18	7	3.3	49	1	TX25_PHONT
19	6	2.8	53	1	LHAL_RIOPAC
20	6	2.8	65	1	MLX_KLEPN
21	6	2.8	97	1	VE2_HPV44
22	6	2.8	101	1	APC2_MACFA
23	6	2.8	110	1	R122_ECOLI
24	6	2.8	111	1	R122_ACHLA
25	6	2.8	112	1	R122_SICCI
26	6	2.8	113	1	R122_THETH
27	6	2.8	115	1	TIAF_HUMAN
28	6	2.8	115	1	TIAF_MOUSE
29	6	2.8	118	1	REV_HVILW
30	6	2.8	119	1	Y13K_NEVOP
31	6	2.8	123	1	RS12_ECOLI
32	6	2.8	131	1	R122_PHRSP1
33	6	2.8	131	1	R122_PHRSP1

ALIGNMENTS

RESULT	1
ELKL_HUMAN	ELKL_HUMAN STANDARD; FRT; 428 AA.
RA	Reddy V. N., Huebner K., Isobe M., Ar-Rushdi A., Croce C. M.,
RA	Reddy E. S. P.,
RT	'elk', tissue-specific ets-related genes on chromosomes X and 14 near
RT	translocation breakpoints.;
RL	Science 244:66-70 (1999).
RN	[1]
RR	SEQUENCE FROM N.A.
RX	Medline=8903250; PubMed=2539641;
RA	Rao V. N., Huebner K., Isobe M., Ar-Rushdi A., Croce C. M.,
RA	Reddy V. N., Huebner K., Isobe M., Ar-Rushdi A., Croce C. M.,
RA	Reddy E. S. P.,
RT	'elk', tissue-specific ets-related genes on chromosomes X and 14 near
RT	translocation breakpoints.;
RL	Science 244:66-70 (1999).
RN	[2]
RR	SEQUENCE FROM N.A.
RX	Medline=99013876; PubMed=9795224;
RA	Harinindrath N., Mills F. C., Mitchell M. P., Meindl A., Max E. E.,
RA	"The human elk-1 gene family: the functional gene and two processed
RT	pseudogenes embedded in the IgH locus.,"
RT	Gene 221:215-224 (1998).
RL	[3]
RR	SEQUENCE FROM N.A.
RA	Graham D.,
RA	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN	[4]
RR	SEQUENCE FROM N.A. (ISOFORM 2).
RA	Aryee D. N. T., Kovar H.;
RA	"Novel family members HUE71, EFLR, and EFLV among ETS-related genes
RT	coexpressed with EWS-FL1 in Ewing tumor cell lines.,"
RT	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RL	[5]
RR	DOMAINS.
RX	Medline=9234979; PubMed=1630933;
RA	Janknecht R., Nordheim A.;
RT	"Elk-1 protein domains required for direct and SRF-assisted
RT	DNA-binding.,"
RL	Nucleic Acids Res. 20:3317-3324 (1992).
CC	-!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC	SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC	FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
CC	ELEMENT.
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.
CC	-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE

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OM protein - protein search, using sw model

Run on: November 9, 2001, 15:47:18 ; Search time 89.8 Seconds
(without alignments)
313.819 Million cell updates/sec

Title: US-09-668-021-10

Score: 213
Sequence: 1 MQLFLALCLVCLVHAFRV KPRPRPARGAKANQAELENAY 213

Scoring table: Oligo
Gapop 60.0 , Gapext 60.0

Search: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 50 summaries

Database : SPTRMBL-16:*

1: SP_archaea:*

2: SP_bacteria:*

3: SP_fungi:*

4: SP_human:*

5: SP_invertebrate:*

6: SP_mammal:*

7: SP_mhc:*

8: SP_oranelle:*

9: SP_phage:*

10: SP_plant:*

11: SP_rodent:*

12: SP_unclassified:*

13: SP_vertebrate:*

14: SP_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	3.8	276 13	Q9YGD6
2	8	3.8	276 13	Q9YGD6 oncorhynchus
3	8	3.8	276 13	Q9PT38 oncorhynchus
4	8	3.8	276 13	Q9PT37 oncorhynchus
5	7	3.3	45 4	Q9HC30 homo sapien
6	7	3.3	89 10	Q9fh55 arabidopsis
7	7	3.3	109 5	Q9GtJ4 arcylostoma
8	7	3.3	114 5	Q9t9K3 manduca sexta
9	7	3.3	125 11	Q9E9Q1 carvia porce
10	7	3.3	130 2	Q9I1C0 pseudomas
11	7	3.3	148 2	Q9HVX4 pseudomonas
12	7	3.3	150 2	Q9E9U6 pasteurella
13	7	3.3	151 2	Q9E9V4 actinobacil
14	7	3.3	151 2	Q9E9Z2 haemophilus
15	7	3.3	151 2	Q9E9Z1 haemophilus
16	7	3.3	151 2	Q9E9Z0 haemophilus
17	7	3.3	151 2	Q9E9Y9 haemophilus
18	7	3.3	151 2	Q9E9Y8 haemophilus
19	7	3.3	151 2	Q9E9Y6 haemophilus

ALIGNMENTS

RESULT	1
ID	Q9YGD6
AC	Q9YGD6;
DT	01-MAY-1999 (TREMBL); 10. Last sequence update)
DT	01-MAR-2001 (TREMBL); 16. (Last annotation update)
DE	CARBOYL REDUCTASE/20BETA HYDROXYSTEROL DEHYDROGENASE B.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Protactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX	NCBL_TaxID=8022;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE:99185307; PubMed:10082666;
RA	Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;
RT	"Cloning and expression of two carboxyl reductase-like 20beta-hydroxy-steroid dehydrogenases cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss)";
RL	Bichem. Biophys. Res. Commun. 255:123-128(1999).
CC	-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
EMBL	AF009390; AAD20217.1; -
DR	HSSP: P50163; 2AEL.
DR	InterPro: IPR02198; -.
DR	InterPro: IPR002347; -.
DR	Pfam: PF00106; aah_short; 1.
DR	PRINTS: PR00081; GDHR01.
DR	PRINTS: PR00080; SDRFAMILY.
KW	oxidoreductase.
SEQUENCE	276 AA; 3011 MW; 135604A38D2940CD CRC64;

Query Match 3.88; Score 8; DB 13; Length 276;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR HSSP; P50163; ZAE1.
 DR InterPro; IPR002198; -.
 DR InterPro; IPR002347; -.
 DR Pfam; PF00106; adh.short; 1.
 DR PRINTS; PRO0081; GDIRDH;
 DR PRINTS; PRO0080; SDRFAMILY.
 DR KW Oxidoreductase.
 SQ SEQUENCE 276 AA; 30127 MW; 1350E421D34225D CRC64;

RESULT 2
 ID 09PT38 PRELIMINARY; PRT; 276 AA.
 AC 09PT38;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE A.
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Protoactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=99185307; PubMed=10082666;
 RA Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;
 RT "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (*Oncorhynchus mykiss*).";
 RL Biochem. Biophys. Res. Commun. 255:123-128(1999).
 CC -i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
 CC FAMILY:
 DR EMBL; AF109931; AAD20992; 1; -.
 DR HSSP; P50163; ZAE1.
 DR InterPro; IPR002198; -.
 DR Intertro; IPR002347; -.
 DR Pfam; PF00106; adh.short; 1.
 DR PRINTS; PRO0080; GDIRDH.
 DR PRINTS; PRO0080; SDRFAMILY.
 KW Oxidoreductase.
 SQ SEQUENCE 275 AA; 30239 MW; 134B52054C751C28 CRC64;

Query Match 3.8%; Score 8; DB 13; Length 276;
 Best Local Similarity 100.0%; Pred. No. 3,3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 ID 09PT37 PRELIMINARY; PRT; 276 AA.
 AC 09PT37;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 OC Protoactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=99185307; PubMed=10082666;
 RA Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;
 RT "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (*Oncorhynchus mykiss*).";
 RL Biochem. Biophys. Res. Commun. 255:123-128(1999).
 CC -i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
 CC FAMILY:
 DR EMBL; AF109931; AAD20218; 1; -.
 DR HSSP; P50163; ZAE1.
 DR Intertro; IPR002198; -.
 DR InterPro; IPR002347; -.
 DR Pfam; PF00106; adh.short; 1.
 DR PRINTS; PRO0080; GDIRDH.
 DR PRINTS; PRO0080; SDRFAMILY.
 KW Oxidoreductase.
 SQ SEQUENCE 276 AA; 30139 MW; 135F1711D30086D CRC64;

Query Match 3.8%; Score 8; DB 13; Length 276;
 Best Local Similarity 100.0%; Pred. No. 3,3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ID 09HC30 PRELIMINARY; PRT; 45 AA.
 AC 09HC30;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE CAMP SPECIFIC PHOSPHODIESTERASE VARIANT PDE4A-10 (FRAGMENT).
 CC PDE4A.
 OC Homo sapiens (Human).
 OS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR EMBL; AF109932; AAD20991; 1; -.

GenCore version 4.5
 Copyright (C) 1993 - 2000 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: November 9, 2001, 15:34:29 ; search time 79.75 Seconds
 (without alignments)
 Word size : 161.917 Million cell updates/sec

Title: US-09-668-021-10
 Perfect score: 213
 Sequence: I MQLPLALCIVCLVHAAFRV KPRPRARGAKANQALENAY 213
 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
 Searched: 412676 seqs, 60623988 residues
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Listing first 50 summaries:
 Database : A_Geneseq_0601:*

1: /SIDS8/gcgtata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgtata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgtata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcgtata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS8/gcgtata/geneseq/geneseqp/AA1984.DAT:*

6: /SIDS8/gcgtata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS8/gcgtata/geneseq/geneseqp/AA1986.DAT:*

8: /SIDS8/gcgtata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS8/gcgtata/geneseq/geneseqp/AA1988.DAT:*

10: /SIDS8/gcgtata/geneseq/geneseqp/AA1989.DAT:*

11: /SIDS8/gcgtata/geneseq/geneseqp/AA1990.DAT:*

12: /SIDS8/gcgtata/geneseq/geneseqp/AA1991.DAT:*

13: /SIDS8/gcgtata/geneseq/geneseqp/AA1992.DAT:*

14: /SIDS8/gcgtata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS8/gcgtata/geneseq/geneseqp/AA1994.DAT:*

16: /SIDS8/gcgtata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS8/gcgtata/geneseq/geneseqp/AA1996.DAT:*

18: /SIDS8/gcgtata/geneseq/geneseqp/AA1997.DAT:*

19: /SIDS8/gcgtata/geneseq/geneseqp/AA1998.DAT:*

20: /SIDS8/gcgtata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS8/gcgtata/geneseq/geneseqp/AA2000.DAT:*

22: /SIDS8/gcgtata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	213	100.0	213	21	AY96431
2	135	63.4	213	21	AAB26106
3	135	63.4	213	21	Human TGF-beta bin
4	135	63.4	213	22	Human TGF-beta bin
5	115	54.0	176	21	Human secreted pro
6	113	53.1	213	21	Bovine TGF-beta bin
7	113	53.1	213	21	Human TGF-beta bin
8	77	36.2	362	21	Human TGF-beta bin
9	33	15.5	50	20	Human TGF-beta bin
10	32	15.0	213	21	Human TGF-beta bin
11	32	15.0	211	21	Human TGF-beta bin

Result No.	Score	Query	Match length	DB ID	Description
1	213	100.0	213	21	AY96431
2	135	63.4	213	21	AAB26106
3	135	63.4	213	21	Human TGF-beta bin
4	135	63.4	213	22	Human secreted pro
5	115	54.0	176	21	Bovine TGF-beta bin
6	113	53.1	213	21	Human TGF-beta bin
7	113	53.1	213	21	Human TGF-beta bin
8	77	36.2	362	21	Human TGF-beta bin
9	33	15.5	50	20	Human TGF-beta bin
10	32	15.0	213	21	Human TGF-beta bin
11	32	15.0	211	21	Human TGF-beta bin

Result No.	Score	Query	Match length	DB ID	Description
12	15	7.0	23	21	AY96431
13	9	4.2	116	18	AAW22654
14	9	4.2	116	18	AAW4090
15	9	4.2	206	18	AAW58704
16	9	4.2	206	19	AAW58711
17	9	4.2	206	21	ARB10233
18	9	4.2	206	21	RAY7581
19	9	4.2	206	21	RAY76031
20	9	4.2	206	22	ARB5520
21	9	4.2	206	22	ARB55910
22	9	4.2	206	22	RAY2704
23	8	4.2	20	21	RAY3294
24	8	3.8	647	19	RAW4833
25	8	3.8	26	21	RAW40943
26	7	3.3	114	19	RAW75569
27	7	3.3	61	21	AAG0348
28	7	3.3	173	21	AY73911
29	7	3.3	99	21	AY68229
30	7	3.3	99	21	AY52883
31	7	3.3	99	22	ARB5644
32	7	3.3	114	21	AYW68387
33	7	3.3	114	19	RAW57845
34	7	3.3	177	20	RAY3001
35	7	3.3	177	20	AYW65018
36	7	3.3	186	19	RAW42285
37	7	3.3	219	21	RAY42285
38	7	3.3	230	21	RAY57845
39	7	3.3	256	20	RAW88386
40	7	3.3	265	21	AAG42284
41	7	3.3	282	21	ANG42283
42	7	3.3	285	21	ARB29625
43	7	3.3	412	19	RAY74207
44	7	3.3	412	19	RAW71369
45	7	3.3	412	20	RAY06418
46	7	3.3	412	21	AYW93695
47	7	3.3	426	22	ARB64892
48	7	3.3	554	20	AYW36226
49	7	3.3	708	20	AYW8383
50	7	3.3	917	18	RAW7437

Result No.	Score	Query	Match length	DB ID	Description
12	15	7.0	23	21	AY96431
13	9	4.2	116	18	AAW22654
14	9	4.2	116	18	AAW4090
15	9	4.2	206	18	AAW58704
16	9	4.2	206	19	AAW58711
17	9	4.2	206	21	RAY7581
18	9	4.2	206	21	RAY76031
19	9	4.2	206	22	ARB5520
20	9	4.2	206	22	ARB55910
21	9	4.2	206	22	RAY2704
22	9	4.2	206	22	RAY3294
23	8	4.2	20	21	RAY3294
24	8	3.8	647	19	RAW4833
25	8	3.8	26	21	RAW40943
26	7	3.3	114	19	RAW75569
27	7	3.3	61	21	AAG0348
28	7	3.3	173	21	AY73911
29	7	3.3	99	21	AY68229
30	7	3.3	99	22	ARB5644
31	7	3.3	114	21	AYW68387
32	7	3.3	114	19	RAW57845
33	7	3.3	114	19	RAW71369
34	7	3.3	177	20	RAY3001
35	7	3.3	177	20	AYW65018
36	7	3.3	186	19	RAW42285
37	7	3.3	219	21	RAY42285
38	7	3.3	230	21	RAY57845
39	7	3.3	256	20	RAW88386
40	7	3.3	265	21	AAG42284
41	7	3.3	282	21	ANG42283
42	7	3.3	285	21	ARB29625
43	7	3.3	412	19	RAY74207
44	7	3.3	412	19	RAW71369
45	7	3.3	412	20	RAY06418
46	7	3.3	412	21	AYW93695
47	7	3.3	426	22	ARB64892
48	7	3.3	554	20	AYW36226
49	7	3.3	708	20	AYW8383
50	7	3.3	917	18	RAW7437

Result No.	Score	Query	Match length	DB ID	Description
12	15	7.0	23	21	AY96431
13	9	4.2	116	18	AAW22654
14	9	4.2	116	18	AAW4090
15	9	4.2	206	18	AAW58704
16	9	4.2	206	19	AAW58711
17	9	4.2	206	21	RAY7581
18	9	4.2	206	21	RAY76031
19	9	4.2	206	22	ARB5520
20	9	4.2	206	22	ARB55910
21	9	4.2	206	22	RAY2704
22	9	4.2	206	22	RAY3294
23	8	4.2	20	21	RAY3294
24	8	3.8	647	19	RAW4833
25	8	3.8	26	21	RAW40943
26	7	3.3	114	19	RAW75569
27	7	3.3	61	21	AAG0348
28	7	3.3	173	21	AY73911
29	7	3.3	99	21	AY68229
30	7	3.3	99	22	ARB5644
31	7	3.3	114	21	AYW68387
32	7	3.3	114	19	RAW57845
33	7	3.3	114	19	RAW71369
34	7	3.3	177	20	RAY3001
35	7	3.3	177	20	AYW65018
36	7	3.3	186	19	RAW42285
37	7	3.3	219	21	RAY42285
38	7	3.3	230	21	RAY57845
39	7	3.3	256	20	RAW88386
40	7	3.3	265	21	AAG42284
41	7	3.3	282	21	ANG42283
42	7	3.3	285	21	ARB29625
43	7	3.3	412	19	RAY74207
44	7	3.3	412	19	RAW71369
45	7	3.3	412	20	RAY06418
46	7	3.3	412	21	AYW93695
47	7	3.3	426	22	ARB64892
48	7	3.3	554	20	AYW36226
49	7	3.3	708	20	AYW8383
50	7	3.3	917	18	RAW7437

Result No.	Score	Query	Match length	DB ID	Description
12	15	7.0	23	21	AY96431
13	9	4.2	116	18	AAW22654
14	9	4.2	116	18	AAW4090
15	9	4.2	206	18	AAW58704
16	9	4.2	206	19	AAW58711
17	9	4.2	206	21	RAY7581
18	9	4.2	206	21	RAY76031
19	9	4.2	206	22	ARB5520
20	9	4.2	206	22	ARB55910
21	9	4.2	206	22	RAY2704
22	9	4.2	206	22	RAY3294
23	8	4.2	20	21	RAY3294
24	8	3.8	647	19	RAW4833
25	8	3.8	26	21	RAW40943
26	7	3.3	114	19	RAW75569
27	7	3.3	61	21	AAG0348
28	7	3.3	173	21	AY73911
29	7	3.3	99	21	AY68229
30	7	3.3	99	22	ARB5644
31	7	3.3	114	21	AYW68387
32	7	3.3	114	19	RAW57845
33	7	3.3	114	19	RAW71369
34	7	3.3	177	20	RAY3001
35	7	3.3	177	20	AYW65018
36	7	3.3	186	19	RAW42285
37	7	3.3	219	21	RAY42285
38	7	3.3	230	21	RAY57845
39	7	3.3	256	20	RAW88386
40	7	3.3	265	21	AAG42284
41	7	3.3	282	21	ANG42283
42	7	3.3	285	21	ARB29625
43	7	3.3	412	19	RAY74207
44	7	3.3	412	19	RAW71369
45	7	3.3	412	20	RAY06418
46	7	3.3	412	21	AYW93695
47	7	3.3	426	22	ARB64892
48	7	3.3	554	20	AYW36226
49	7	3.3	708	20	AYW8383
50	7	3.3	917	18	RAW7437

Result No.	Score	Query	Match length	DB ID	Description
12	15	7.0	23	21	AY96431
13	9	4.2	116	18	AAW22654
14	9	4.2	116	18	AAW4090
15	9	4.2	206	18	AAW58704
16	9	4.2	206	19	AAW58711
17	9				

DR	N-PSDB: AAA29057.
XX	Nucleic acids ('1') encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
PT	
PT	
XX	Claim 4; Page 122-123; 162pp; English.
XX	
CC	This shows a <i>vervet</i> transforming growth factor-beta (TGF-beta) binding protein designated vBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patient's own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
CC	
CC	Sequence 213 AA;
CC	Query Match 100.0%; Score 213; DB 21; Length 213;
CC	Best Local Similarity 100.0%; Pred. No. 4; 3e-214; Mismatches 0; Indels 0; Gaps 0
CC	Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CC	1 mqplialcivclvhaafkrvveggwgqafkndateipelgeypepppelennkthmra 60
CC	1 mqplialcivclvhaafkrvveggwgqafkndateipelgeypepppelennkthmra 60
CC	61 NGGRPHPHPETKSYKSESCRELFTRYTGDGCRSAKPVTEVCSQCGQPARILPAIG 120
CC	61 ngrgrphphpetkdysevsscrelftrytgdgcrsakpvtevcsqcgqparilphaig 120
CC	61 ngrgrphphpetkdysevsscrelftrytgdgcrsakpvtevcsqcgqparilphaig 120
CC	121 RGKWRPSPGDFRCIPDRRAQRQVQLQCPGGAPRARRVVRUVASCKRKLTRFHNGSELK 180
CC	121 rgkwrpsgsdpdfrcipdrqraqvqyqllcpqgaaprarkvrlavascckrkltrfhngselk 180
CC	181 DFGPBAARPOKGRIKPRPRAGAKANQAELENAY 213
CC	181 dfgpbaarpqkgrprprargakanqaeleinay 213
XX	
RESULT	2
ID	AAB26106
XX	AAB26106 standard; protein; 213 AA.
AC	AAB26106;
XX	
DT	15-JAN-2001 (first entry)
XX	
DE	Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and 4).
XX	
KW	Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein; antagonist; BMP; cell growth; cell differentiation; bone formation; gene therapy.
KW	
XX	
OS	<i>Homo sapiens</i> .
XX	
PN	WO200055193-A2.
XX	
PD	21-SEP-2000.
XX	
PF	02-MAR-2000; 2000WO-US05537.
XX	
PR	12-NAR-1999; 99US-0124118.
XX	
PA	(REGE-) REGENERON PHARM INC.

XX
 PI Economides AN:
 XX
 DR WPI; 2000-638179/61.
 XX
 DR N-PSDB; AAA94051.
 XX
 PT Novel isolated, human DNA/Cerberus related protein 6 which include
 natural homologue, and polypeptides comprising DCR6 domain and nucleic
 acids encoding the proteins which are useful as probes and primers -
 XX
 PS Claim 8; Fig 3; 40PP; English.
 XX
 CC The present sequence comprises the amino acid sequence encoded by exons 1
 and 4 of the human DAN/Cerberus-related protein 6 (hDCR6) coding
 sequence. The coding sequence was isolated from a human kidney cDNA
 library containing exons 1 and 4 of the sequence. hDCR6 is closely
 related to the DAN and DCR5 proteins, both of which act as antagonists of
 morphogenic proteins such as BMP. It is possible that the hDCR6 gene and
 protein can be used as immunogens, modulators of cell function, growth
 and differentiation, to reduce undesirable bone formation, to identify
 DCR6 binding agents, in diagnosis, and in gene therapy.
 XX
 SQ Sequence 213 AA:

RESULT	3
AY96429	63.4%; Score 135; DB 21; Length 213;
Best Local Similarity	100.0%; Pred. No. 9.7e-133;
Matches	135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	17 AFRVVEGQSMQAFKDATEIPELGEYPPPEPLNNKNTKRNRAENGGRPPHHPFENKDS 76
Db	17 afrvvegqwgafkndateiipelgeypppeplnnkntkrnraenggrpphhpfekds 76
QY	77 EYSCRELHFRYVWDGPGCSAKPVTELVCQGQCARLNAIGGKWWRPSGPFRCIP 136
Db	77 eyscrelhfrtyvdgpcrsakpvtelvcsgqgqcparlbnraiggrgkwwrpsgpfrcip 136
QY	137 DRYRAQRVQLICPGG 151
Db	137 dryraqrqyq1lcpgg 151

XX
 AAY96429 standard; Protein; 213 AA.
 XX
 AC AAY96429;
 XX
 DT 12-SEP-2000 (first entry)
 XX
 DE Human TGF-beta binding protein (BEER).
 XX
 KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
 KW BEER; gene therapy; antisense therapy; fracture; bone mineralization.
 XX
 OS Homo sapiens.
 XX
 PN WO200032773-A1.
 XX
 PD 08-JUN-2000.
 XX
 PP 24 -NOV-1999; 99WO-US27990.
 XX
 PR 27 -NOV-1998; 98US 0110283.
 XX
 PA (DARW-) DARWIN DISCOVERY LTD.
 XX
 PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JR, Paeper BW;
 PI Van Ness J, Winkler DG;
 XX
 DR WPI; 2000-412321/35.
 DR N-PSDB; AAA29055.

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:35:23 ; Search time 47.66 Seconds
(without alignments)
100.571 Million cell updates/sec

Title: US-09-668-021-10
Perfect score: 213
Sequence: 1 MQLLALCLVLVHAAFRV. KPRPRARGAKANQAELENAY 213

Scoring table: Oligo Gap 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 50 summaries

Database : Issued_Patents_AA:*

1: /ccn2_6/ptodata/2/iaa/5A_COMB_pep:*

2: /ccn2_6/ptodata/2/iaa/5B_COMB_pep:*

3: /ccn2_6/ptodata/2/iaa/6A_COMB_pep:*

4: /ccn2_6/ptodata/2/iaa/6B_COMB_pep:*

5: /ccn2_6/ptodata/2/iaa/PCNUS_COMB_pep:*

6: /ccn2_6/ptodata/2/iaa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match Length	DB ID	Description
1	9	4.2	206	1	US-08-468-847B-2
2	9	4.2	206	1	US-08-468-847B-2
3	9	4.2	206	1	US-08-468-847B-2
4	9	4.2	206	4	US-09-188-930-286
5	8	3.8	647	3	US-08-153-007A-32
6	7	3.3	8	4	US-09-398-946-32
7	7	3.3	99	2	US-08-484-905-61
8	9	3	US-08-481-985B-61		
9	7	3.3	99	3	US-08-370-476-61
10	7	3.3	114	1	US-08-592-257-15
11	7	3.3	114	2	US-08-592-288-15
12	7	3.3	186	4	US-09-475-316A-13
13	7	3.3	412	1	US-08-208-007A-12
14	7	3.3	412	4	US-08-974-691-4
15	7	3.3	861	1	US-08-764-100-24
16	7	3.3	917	2	US-08-888-983-16
17	7	3.3	917	2	US-08-888-976-16
18	6	2.8	39	3	US-08-554-305-22
19	6	2.8	68	2	US-08-836-871-5
20	6	2.8	80	1	US-08-011-338B-15
21	6	2.8	80	1	US-08-64-051-15
22	6	2.8	80	1	US-08-62-498-15
23	6	2.8	80	3	US-08-554-305-14
24	6	2.8	88	2	US-08-630-011A-31
25	6	2.8	97	2	US-08-245-511-30
26	6	2.8	97	2	US-08-600-933A-30
27	1	US-08-225-989-20			

ALIGNMENTS

RESULT 1
US-08-468-847B-2
; Sequence 2, Application US/08468847B
; Patent No. 578023
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; ;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468-847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33-073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-468-847B-2

Query Match 4.2%; Score 9; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.37; Title of Invention: Compositions Isolated From Skin Cells
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Number of Sequences: 20

QY 28 AFKNDATEI 36
 Db 23 AFKNDATEI 31

RESULT 2
 US-08-468-847B-20
 Sequence 20, Application US/08468847B

GENERAL INFORMATION:
 APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 TITLE OF INVENTION: Human CCN-Like Growth Factor
 NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ADDRESSE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,847B
 FILING DATE: 6 June 1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33 073
 REFERENCE/DOCKET NUMBER: 325800-442

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 205 AMINO ACIDS
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-468-847B-20

Query Match 4.2%; Score 9; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.37; Title of Invention: Compositions Isolated From Skin Cells
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Number of Sequences: 20

QY 28 AFKNDATEI 36
 Db 23 AFKNDATEI 31

RESULT 4
 US-09-188-930-286
 Sequence 286, Application US/09188930A

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Murison, James Greg
 APPLICANT: Onrust, Rene

CURRENT APPLICATION NUMBER: US/09/188,930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206
 TYPE: PRT
 ORGANISM: Mouse

Query Match 4.2%; Score 9; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.37; Title of Invention: Compositions Isolated From Skin Cells
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Number of Sequences: 33

QY 28 AFKNDATEI 36
 Db 23 AFKNDATEI 31

RESULT 5
 US-08-75-007A-32
 Sequence 32, Application US/08753007A

GENERAL INFORMATION:
 PATENT NO. 6074841
 APPLICANT: Gearing, David P.
 APPLICANT: Busfield, Samantha J.
 TITLE OF INVENTION: D0N-1 GENE AND POLYPEPTIDES
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

Query Match 4.2%; Score 9; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.37; Title of Invention: D0N-1 GENE AND POLYPEPTIDES
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Number of Sequences: 33

QY 28 AFKNDATEI 36
 Db 23 AFKNDATEI 31

GENERAL INFORMATION:
 PATENT NO. 6150502
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Murison, James Greg
 APPLICANT: Onrust, Rene

CURRENT APPLICATION NUMBER: US/09/188,930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206
 TYPE: PRT
 ORGANISM: Mouse

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:36:28 ; Search time 54.37 seconds

(without alignments) 295.619 Million cell updates/sec

Title: US-09-668-021-12
Perfect score: 211
Sequence: 1 MQPSLAPCLICLIVHAAFCA.....KPRPGARGAKANQAELENAY 211

Scoring table: ORIGO Gapop 60.0 , Gapext 60.0

arched: 219241 seqs, 76174552 residues

word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : PIR 58.0
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.8	428	1 TVHUEK	transforming protein
2	8	3.8	429	2 JC1965	elk1 protein - mouse
3	7	3.3	99	1 MGGB2	beta-2-microglobulin
4	7	3.3	130	2 DB8305	hypothetical protein
5	7	3.3	148	2 C83091	hypothetical protein
6	7	3.3	197	2 G81057	hypothetical protein
7	7	3.3	197	2 A81819	hypothetical protein
8	7	3.3	222	2 B41643	urokinase-type plasminogen activator
9	7	3.3	222	2 B53356	urokinase-type plasminogen activator
10	7	3.3	321	2 B82892	conserved hypothetical protein
11	7	3.3	327	2 A55356	urokinase-type plasminogen activator
12	7	3.3	328	2 S42152	urinary plasminogen activator
13	7	3.3	328	2 S72647	hypothetical protein
14	7	3.3	354	2 C83577	hypothetical protein
15	7	3.3	398	1 S24802	polyferredoxin 6x2
16	7	3.3	531	2 B83082	probable binding protein
17	7	3.3	535	1 A83194	periplasmic diphopeptides
18	7	3.3	541	2 T45617	transmembrane protein
19	7	3.3	542	2 T23869	hypothetical protein
20	7	3.3	562	2 T05758	hypothetical protein
21	7	3.3	565	2 B70652	probable cytoskeletal protein
22	7	3.3	632	1 VGYNSY	surface glycoprotein
23	7	3.3	681	2 E82812	outer membrane hem
24	7	3.3	836	2 B84417	cell surface glycoprotein
25	7	3.3	852	2 A84592	cell surface glycoprotein
26	7	3.3	1168	1 MWAXIC	myosin heavy chain
27	7	3.3	1308	2 T15280	hypothetical protein
28	7	3.3	1940	2 A59287	myosin heavy chain

RESULT 1
TVHUEK
transforming protein elk-1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: AA1354; S54721
R;Rao, V.N.; Huebner, K.; Isobe, M.; arrushdi, A.; Croce, C.M.; Reddy, E.S.P.
Science 241, 66-70, 1989
A;Title: elk, tissue-specific ets-related genes on chromosomes X and 14 near transloc
A;Reference number: AA1354; MUID:89203250
A;Accession: AA1354
A;Molecule type: mRNA
A;Residues: 1-428 <RAO>
A;Cross-references: GB: M25269; PIDN: AAA52384.1; PID: 9538209
R;Grevin, H.; Kortenjann, M.; Thomas, O.; Moomaw, C.; Slaughter, C.; Cobb, M.H.; Shaw, EMBO J. 14, 951-962, 1995
A;Title: Elk phosphorylation potentiates Elk-1-mediated ternary complex formation and
A;Reference number: S54721; MUID: 95196758
A;Accession: S54721
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 318-328, 'XX', 331:336-364; 380-388, 'X', 390-392, 'X', 394-400, 'XX', 403-405, 'X'
C;Genetics:
A;Gene: GDB:ELK1
A;Cross-references: GDB:119867; OMIM:311040
A;Map position: xpl1-2-xpl1.2
C;Superfamily: elk-1-transforming protein; ets DNA-binding domain homology
C;Keywords: DNA binding; oncogene; transforming protein
P;7-86/Domain: ets DNA-binding domain homology <ETs>

ALIGNMENTS

Query Match 3.8%; Score 8; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 PQKGRKPR 194
Db 310 PQKGRKPR 317

RESULT 2
JC4965
elk1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C;Accession: JC4965; I48339; I48340; S54908
R;Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin, D.

Gene 174, 185-188, 1996
 A; Title: Structure and organization of the mouse elkl gene.
 A; Reference number: JC4965; MUID:97017146
 A; Molecule type: mRNA
 A; Residues: 1-429 <GRE>
 A; Cross-references: EMBL:AB7257; NID:9836634; PIDN:CAA60715.1; PID:9836635
 A; Experimental source: embryo
 R; Giobane, A.; Pintas, A.; Maira, S.M.; Sobleszczuk, P.; Wasyluk, B.
 Genes Dev. 8, 1502-1513, 1994
 A; Title: Net, a new ets transcription factor that is activated by Ras.
 A; Reference number: A53837; MUID:95047310
 A; Accession: 1A8340
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: mRNA
 A; Residues: 1-429 <STO>
 A; Cross-references: EMBL:XB7257; NID:9836634; PIDN:CAA60715.1; PID:9836635
 A; Gene: elkl
 A; Introns: 70/3; 219/3; 363/3; 397/3
 C; Superfamily: ets; DNA-binding domain homology <ETS>
 R; 7-86/Domain: ets DNA-binding domain homology <ETS>
 Query Match 3.8%; Score 8; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 8; Conservative 0; Indels 0; Gaps 0; Matches 0;
 Qy 187 POKGRKR 194
 ||||| |||||
 Db 311 POKGRKR 318
 RESULT 3
 MGFB2
 beta-2-microglobulin - guinea pig
 N: Alternate names: class I histocompatibility antigen beta chain
 C: Species: *Canis porcellus* (guinea pig)
 C: Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Jan-1997
 C: Accession: A02181
 R; Wolfe, P.B.; Cebara, J.J.
 Mol. Immunol. 17, 1403-1505, 1980
 A; Title: The primary structure of guinea pig beta2-microglobulin.
 A; Reference number: A02181; MUID:82057805
 A; Accession: A02181
 A; Molecule type: protein
 A; Residues: 1-99 <WON>
 C; Complex: heterodimer with MHC class I histocompatibility antigen alpha chain
 C; Function:
 A; Description: necessary for the expression of MHC class I histocompatibility antigen
 C; Superfamily: immunoglobulin C region; immunoglobulin homology
 C; Keywords: heterodimer
 F; 18-82/Domain: immunoglobulin homology <IMM>
 F; 25-80/disulfide bonds: #status predicted
 RESULT 4
 Query Match 3.3%; Score 7; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 11; Mismatches 7; Conservative 0; Indels 0; Gaps 0; Matches 0;
 Qy 12 LLVHAAF 18
 |||||
 Db 64 LLVHAAF 70
 RESULT 4
 Query Match 3.3%; Score 7; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 11; Mismatches 7; Conservative 0; Indels 0; Gaps 0; Matches 0;
 Qy 110 ARLLPNA 116
 |||||
 Db 26 ARLLPNA 32
 RESULT 5
 C83091
 hypothetical protein PA4441 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C; Species: *Pseudomonas aeruginosa*
 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C; Accession: C83091
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoduchi, S.D.; Warrener, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lachig, K.; L.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A; Reference number: A82950; MUID:20437337
 A; Accession: C83091
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-148 <STO>
 A; Cross-references: GB:AE004858; PIDN:AE004091; NID:99950668; PIDN:AAG07829.1; GSPDB:GN
 A; Experimental source: strain PA01
 A; Genetics:
 A; Gene: PA4441
 RESULT 6
 G81057
 hypothetical protein NMB1556 [imported] - *Neisseria meningitidis* (strain MC58 serogroup C)
 C; Species: *Neisseria meningitidis*
 C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C; Accession: G81057
 R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Halt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.; Hui, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287, 1803-1815, 2000
 A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A; Reference number: A81000; MUID:20175755

Result No.	Score	Query	Match Length	DB ID	Description
1	8	8	3.8	1	ELK1_HUMAN
2	8	8	3.8	1	ELK1_MOUSE
3	7	3	3.3	1	VE7_HPV4
4	7	3	3.3	1	B2NG_CAVPO
5	7	3	3.3	1	RL22_ELPIN
6	7	3	3.3	220	1 UPAS_RAT
7	7	3	3.3	222	1 UPAS_MOUSE
8	7	3	3.3	281	1 PAB4_ECOLI
9	7	3	3.3	327	1 UPAR_MOUSE
10	7	3	3.3	328	1 UPAR_RAT
11	7	3	3.3	535	1 DPRA_ECOLI
12	7	3	3.3	632	1 VGLG_STNV
13	7	3	3.3	852	1 CSG_HA1HA
14	7	3	3.3	1168	1 MYC_ACACA
15	6	2	2.8	49	1 TX25_PHONEUTRIA
16	6	2	2.8	53	1 LRA1_RHOAC
17	6	2	2.8	107	1 TH12_CORNE
18	6	2	2.8	110	1 RL22_ECOLI
19	6	2	2.8	111	1 RL22_ACHLA
20	6	2	2.8	112	1 RL22_SICLI
21	6	2	2.8	113	1 RL22_TRETH
22	6	2	2.8	115	1 TIAF_HUMAN
23	6	2	2.8	115	1 TIAF_MOUSE
24	6	2	2.8	118	1 REV_HVILLW
25	6	2	2.8	131	1 RL22_PHYS1
26	6	2	2.8	145	1 SYNL_RAT
27	6	2	2.8	167	1 BAR_MURIN
28	6	2	2.8	173	1 FRIS_LMST
29	6	2	2.8	182	1 YCYO_YEAST
30	6	2	2.8	193	1 HS72_CNA1
31	6	2	2.8	196	1 REPB_CHICK
32	6	2	2.8	204	1 BAD_MOUSE
33	6	2	2.8	210	1 TRPF_KLULKA

ALIGMENTS					
34	6	2.8	213	1	PYRE_HAETN
35	6	2.8	216	1	FGFH_HUMAN
36	6	2.8	216	1	FGFH_MOUSE
37	6	2.8	227	1	PRL_HUMAN
38	6	2.8	227	1	PRL_MACMU
39	6	2.8	230	1	COX2_BRAFL
40	6	2.8	239	1	COX2_BRALIA
41	6	2.8	245	1	DAPB_MYCTU
42	6	2.8	249	1	APX1_PEA
43	6	2.8	261	1	DHSB_RICPCR
44	6	2.8	263	1	LEF5_NPVP0
45	6	2.8	267	1	DAPB_BACSU
46	6	2.8	269	1	ESL1_MYCPN
47	6	2.8	272	1	THM_BACSU
48	6	2.8	280	1	HES1_HUMAN
49	6	2.8	281	1	HES1_RAT
50	6	2.8	282	1	HES1_MOUSE

RESULT	1	ELK1_HUMAN	STANDARD; PRT; 428 AA.
ID	ELK1_HUMAN		
AC	P19419; O75606; Q9UUM4; 095058;		
DT	01-NOV-1990 (Rel. 16, Created)		
DT	01-OCT-2000 (Rel. 40, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	ETS-DOMAIN PROTEIN ELK-1.		
GN	ELK1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX			
RN	[1] NCBI_TAXID=9606;		
RP	SEQUENCE FROM N.A.		
RA	RA Reddy B.S.P.; Recu V.N., Huebner K., Isobe N., Ar-Rushdi A., Croce C.M.,		
RT	RT "Elk, tissue-specific ets-related genes on chromosomes X and 14 near translocation breakpoints." ; Science 244:66-70(1989).		
RL			
RN	RP SEQUENCE FROM N.A.		
RX	RA Harindranath N., Mills F.C., Mitchell M.P., Meindl A., Max E.E.; RT "The human elk-1 gene family: the functional gene and two processed pseudogenes embedded in the IgH locus." ; RL Gene 221:215-224(1998).		
RN	RP SEQUENCE FROM N.A.		
RA	RA Graffham D.; RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.		
RN	RA [4] SEQUENCE FROM N.A. (ISOFORM 2).		
RP	RA Arvey D.N.T., Kovar H.; RT "Novel family members HuER71, EFLR, and ELKv among ETS-related genes coexpressed with EWS-FLI1 in Ewing tumor cell lines." ; RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.		
RA	RA [5] DOMAINS.		
RP	RA Janknecht R., Nordheim A.; RT "Elk-1 protein domains required for direct and SRF-assisted DNA-binding." ; RL Nucleic Acids Res. 20:3317-3324 (1992).		
CC	CC -1- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.		
CC	CC -1- SUBCELLULAR LOCATION: NUCLEAR.		
CC	CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE		

CC	PRODUCED BY ALTERNATIVE SPLICING.	RL	Genes Dev. 8:1502-1513(1994).
CC	-1- TISSUE SPECIFICITY: LUNG AND TESTIS.	CC	-1- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
CC	-1- PTM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK, AND ERK).	CC	SEQUENCES CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
CC	-1- SIMILARITY: BELONGS TO THE ETS FAMILY.	CC	FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
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CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	SUBCELLULAR LOCATION: NUCLEAR.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	LEMMONY: BELONGS TO THE ETS FAMILY.
DR	EMBL; M25269; AAA52384_1; -.	DR	EMBL; X87257; CAA0715_1; -.
DR	EMBL; AF080616; AAC82466_1; -.	DR	EMBL; 236939; CA85391_1; -.
DR	EMBL; AL008172; CAA15659_1; -.	DR	HSSP; P14921; 257W.
DR	EMBL; AF000672; AAD00862_1; -.	DR	MGI; MG1:101833; Elk1.
DR	PIR; A41354; THUEK.	DR	InterPro; IPR00418; -.
DR	HSSP; P14921; 257W.	DR	PFam; PF00178; ETS; 1.
DR	TRNSTRAC; T00250; -.	DR	PRINTS; PRO054; ETSDOMAIN.
DR	MIN; 311040; -.	DR	PROSITE; PS00454; ETS_DOMAIN_1; 1.
DR	InterPro; IPR00418; -.	DR	PROSITE; PS00456; ETS_DOMAIN_2; 1.
DR	PFam; PF00178; Ets; 1.	DR	PROSITE; PS00457; ETS_DOMAIN_3; 1.
DR	PRINTS; PRO054; ETSDOMAIN.	DR	KW TRANSCRIPTION regulation; Activator; Nuclear protein; DNA-binding; Phosphorylation.
DR	PROSITE; PS00345; ETS_DOMAIN_1; 1.	DR	DR PROSITE; PS00561; ETS_DOMAIN_3; 1.
DR	PROSITE; PS00346; ETS_DOMAIN_2; 1.	DR	KW TRANSCRIPTION regulation; Activator; Nuclear protein; DNA-binding; Phosphorylation.
DR	PROSITE; PS00061; ETS_DOMAIN_3; 1.	DR	DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR	KW Phosphorylation; Alternative splicing.	DR	DNA_BIND 5
FT	VARSPLIC 91 95 VAGCS->SHCAP (IN ISOFORM 2).	FT	CONFLICT 133 133 P -> T (IN REF. 2).
FT	VARSPLIC 96 428 MISSING (IN ISOFORM 2).	FT	SEQUENCE 429 AA; 45243 MW; B6185B97731D54F CRC64;
FT	VARSPLIC 183 183 S -> N (IN REF. 1).	FT	Query Match 3.8%; Score 8; DB 1; Length 429;
FT	SEQUENCE 428 AA; 44888 MW; 68F71F8ADB9D386CA CRC64;	FT	Best Local Similarity 100.0%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	187 PQKGRKPR 194	Qy	187 PQKGRKPR 194
Db	310 PQKGRKPR 317	Db	311 PQKGRKPR 318
RESULT 3		RESULT 3	
VE7_HPV4 2	VE7_HPV4 4	VE7_HPV4 2	VE7_HPV4 4
ID EULK1_MOUSE STANDARD; PRN; 429 AA.	ID EULK1_MOUSE STANDARD; PRN; 429 AA.	ID EULK1_MOUSE STANDARD; PRN; 429 AA.	ID EULK1_MOUSE STANDARD; PRN; 429 AA.
AC P41969; 32, Created	AC P41969; 32, Created	AC P41969; 32, Created	AC P41969; 32, Created
DT 01-NOV-1995 (Rel. 32, Last sequence update)	DT 01-NOV-1995 (Rel. 32, Created)	DT 15-JUL-1998 (Rel. 36, Last sequence update)	DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)	DT 01-OCT-1996 (Rel. 34, Last sequence update)	DT 15-JUL-1998 (Rel. 36, Last annotation update)	DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ETS-DOMAIN PROTEIN ELK-1.	DE ETS-DOMAIN PROTEIN ELK-1.	DE E7 PROTEIN.	DE E7 PROTEIN.
GN E7.	GN E7.	GN E7.	GN E7.
OS Human papillomavirus type 44.	OS Human papillomavirus type 44.	OS Human papillomavirus type 44.	OS Human papillomavirus type 44.
OC Papovaviridae; Papovaviridae; Papovaviridae; Papovaviridae.	OC Papovaviridae; Papovaviridae; Papovaviridae; Papovaviridae.	OC Papovaviridae; Papovaviridae; Papovaviridae; Papovaviridae.	OC Papovaviridae; Papovaviridae; Papovaviridae; Papovaviridae.
OC Mammalia; Butherida; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Mammalia; Butherida; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Mammalia; Butherida; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Mammalia; Butherida; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TAXID:10090;	OX NCBI_TAXID:10090;	OX NCBI_TAXID:10090;	OX NCBI_TAXID:10090;
RN [1]	RN [1]	RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Embryo;	RC STRAIN=C57BL; TISSUE=Embryo;	RC STRAIN=C57BL; TISSUE=Embryo;	RC STRAIN=C57BL; TISSUE=Embryo;
RX MEDLINE=9701716; PubMed=8833747;	RX MEDLINE=9701716; PubMed=8833747;	RX MEDLINE=9701716; PubMed=8833747;	RX MEDLINE=9701716; PubMed=8833747;
RA Grevin D., Ung S., Denhez F., Dehem M., Quatannens B., Begue A., Schefelin D., Martin P.;	RA Grevin D., Ung S., Denhez F., Dehem M., Quatannens B., Begue A., Schefelin D., Martin P.;	RA Grevin D., Ung S., Denhez F., Dehem M., Quatannens B., Begue A., Schefelin D., Martin P.;	RA Grevin D., Ung S., Denhez F., Dehem M., Quatannens B., Begue A., Schefelin D., Martin P.;
RL Gene 174:185-188(1996).	RL Gene 174:185-188(1996).	RL Gene 174:185-188(1996).	RL Gene 174:185-188(1996).
RN [2]	RN [2]	RN [2]	RN [2]
RP SEQUENCE OF 5-224 FROM N.A.	RP SEQUENCE OF 5-224 FROM N.A.	RP SEQUENCE OF 5-224 FROM N.A.	RP SEQUENCE OF 5-224 FROM N.A.
RC TISSUE=Embryo;	RC TISSUE=Embryo;	RC TISSUE=Embryo;	RC TISSUE=Embryo;
RX MEDLINE=95047310; PubMed=7958835;	RX MEDLINE=95047310; PubMed=7958835;	RX MEDLINE=95047310; PubMed=7958835;	RX MEDLINE=95047310; PubMed=7958835;
RA Giovane A., Pintzas A., Maira S.-M., Sobieszcuk R., Wasyluk B.; Net, a new ets transcription factor that is activated by Ras.;	RA Giovane A., Pintzas A., Maira S.-M., Sobieszcuk R., Wasyluk B.; Net, a new ets transcription factor that is activated by Ras.;	RA Giovane A., Pintzas A., Maira S.-M., Sobieszcuk R., Wasyluk B.; Net, a new ets transcription factor that is activated by Ras.;	RA Giovane A., Pintzas A., Maira S.-M., Sobieszcuk R., Wasyluk B.; Net, a new ets transcription factor that is activated by Ras.;

				GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.				
OM protein - protein search, using sw model				
Run on: November 9, 2001, 15:47:18 ; Search time 89.8 Seconds				
perfect score: 211				(without alignments)
Sequence: 1 MOP\$AFCILCLVHAAFC...KPRP\$ARGAKANQAELENAY 211				310.873 Million cell updates/sec
Scoring table: OLIGO				
Word size : 0				
Total number of hits satisfying chosen parameters: 425026				
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Post-processing: Listing first 50 summaries				
Database : SPREMBL_16:*				
1: sp_archea:*				
2: sp_bacteria:*				
3: sp_fungi:*				
4: sp_human:*				
5: sp_invertebrate:*				
6: sp_mammal:*				
7: sp_mic:*				
8: sp_organelle:*				
9: sp_phage:*				
10: sp_plant:*				
11: sp_rabbit:*				
12: sp_uniclassified:*				
13: sp_vertebrate:*				
14: sp_virus:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	7	3.3	89	09FH55
2	7	3.3	109	09GTJ4
3	7	3.3	125	11Q9E0Q1
4	7	3.3	130	2Q91OC0
5	7	3.3	148	2Q9HMX4
6	7	3.3	197	2Q9JYB9
7	7	3.3	197	2Q9JTA0
8	7	3.3	208	2Q93581
9	7	3.3	239	14Q9IBJ1
10	7	3.3	251	2Q9L1NO
11	7	3.3	278	2Q9KZ52
12	7	3.3	282	10Q9XF19
13	7	3.3	321	2Q9PQ72
14	7	3.3	322	11Q9R119
15	7	3.3	328	11Q95771
16	7	3.3	345	10Q9FNU1
17	7	3.3	354	2Q915Y7
18	7	3.3	362	2Q9RJX3
19	7	3.3	365	10Q9LG89
RESULT 1				
Q9FH55				PRELIMINARY; PRT; 89 AA.
ID Q9FH55				
AC Q9FH55;				
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				
DE GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K1120.				
OS Arabidopsis thaliana (Mouse-ear cress).				
OC Eukaryota; Viriplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX NCBI_TaxID:3702.				
RN [1]				
RP SQUENCE FROM N A.				
RC STRAIN=COLUMBIAN				
RX MEDLINE=20181125; PubMed=10718197;				
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H., Tabata S.,				
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty PI and TAC clones"; DNA Res. 7, 31-65 (2000).				
RT DNA Res. 7, 31-65 (2000).				
RL AB02211; BAB1013.1; -.				
DR EMBL: AB02211; BAB1013.1; -.				
SO SEQUENCE: 89 AA; 10345 MW; DF123344C936FAE0A CRC64;				
RESULT 2				
Query Match 3.3%; Score 7; DB 10; Length 89;				
Best Local Similarity 100.0%; Pred No. 13; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 111 RLLPNAI 117				
Db 18 RLLPNAI 24				

Q9GTJ4	PRELIMINARY;	PRT;	109 AA.	OX
ID Q9GTJ4				RN [1]
AC Q9GTJ4;				RP SEQUENCE FROM N.A.
DT 01-MAR-2001 (TREMBLrel. 16, Created)				STRAIN=PA01;
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				RX MEDLINE=20437337; PubMed=10984043;
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				RA Stover C.R., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.
DE ZINC METALLOPROTEASE 3 MEP3 (FRAGMENT).				RA Hickey M.J., Brinkman F.S.L., Hurlage W.O., Kowalik D.J., Lagrou M.,
OS Ancylostoma caninum (dog hookworm).				RA Garber R.L., Coltrry L., Tolentino E., Westbroek-Wagman S., Yuan Y.,
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;				RA Brody L.I., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
OC Ancylostomatidae; Ancylostomatinae; Ancylostoma.				RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
OC NCBI_TAXID=29170;				RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.,
RN [1]				RT "Complete genome sequence of <i>Pseudomonas aeruginosa</i> PA01, an
RC TISSUE=WHOLE WORMS;				RT opportunistic pathogen.;"
RA Jones B.F., Hotez P.J.;				RL Nature 406:959-964(2000).
RT "Cloning and characterization of a zinc-metalloprotease secreted by				DR EMBL; AE00470; AAG06110.1; -.
RT the invasive stages of <i>Ancylostoma caninum</i> ;"				KW Hypothetical protein.
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.				SO SEQUENCE 109 AA; 12300 MW; ECEDBCD7F247836E CRC64;
FT NON_TER 1				Query Match 3.3%; Score 7; DB 5; Length 109; Qy 156 KVRLVVAS 162
SEQUENCE				Best Local Similarity 100.0%; Pred. No. 15; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 12 KVRLVVAS 18
QY 129 DFRGCPD 135				RESULT 5
Db 86 DFRGCPD 92				Query Match 3.3%; Score 7; DB 2; Length 130; Qy 156 KVRLVVAS 162
RESULT 3				Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 12 KVRLVVAS 18
Q9EQQ1	PRELIMINARY;	PRT;	125 AA.	RESULT 4
ID Q9EQQ1				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
AC Q9EQQ1;				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
DT 01-MAR-2001 (TREMBLrel. 16, Created)				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
DE BETA2 MICROGLOBULIN.				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
OS Cavia porcellus (Guinea pig);				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi; Cavia.				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
OC NCBI_TAXID=10141;				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
RN [1]				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
RP SEQUENCE FROM N.A.				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
RA LeClair K.P., Naylor J.W., Kawasaki E.;				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
RA Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
DR SEQUENCE 125 AA; 13977 MW; 3F3224B02F0B41C3 CRC64;				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
QY Query Match 3.3%; Score 7; DB 11; Length 125; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OX NCBI_TaxID=287;				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
Db 12 LIVHAF 18				Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
Db 90 LIVHAF 96				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
RESULT 4				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
Q9I0CO	PRELIMINARY;	PRT;	130 AA.	RESULT 6
ID Q9I0CO				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
AC Q9I0CO;				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
DT 01-MAR-2001 (TREMBLrel. 16, Created)				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
DE HYPOTHETICAL PROTEIN PA2722.				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
GN PA2722.				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
OS Pseudomonas aeruginosa.				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				Query Match 3.3%; Score 7; DB 2; Length 148; Qy 110 ARLPNA 116
OC Pseudomonas.				Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DB 26 ARLPNA 32

DR N-PSDB: AAA29058. PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
 XX PT Van Ness J, Winkler DC;
 PT WPI: 2000-412321/35. XX
 PT N-PSDB: AAA22059. DR
 XX PS Claim 5; Page 124; 162pp; English. XX
 XX This shows a murine transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures. DR
 CC CC inappropriately. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patient's own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content. XX
 CC CC Sequence 211 AA; XX

Query Match 100 %; Score 211; DB 21; Length 211;
 Best Local Similarity 100 %; Pred. No. 2.3e-210; Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX

QY 1 MOPSLAPCLCLLVHAFCLVEGQWQAFRRNDATEVIFGLGEVPEPPENOTMNRANG 60
 Db 1 mqpslpcilclvnafcveggwgarnndatevifglgevpeppenqtmraeng 60
 QY 61 GRPHPHYDAKDVSEYSCRLLHYTRFLTUGPCRSKAPVYPTELVCSGQCGPARLIPNAGRV 120
 Db 61 grphphypydkdvsycrelytfltdgpcrskakptelvsgqgcpalpnlagnrv 120
 QY 121 KWWRPNGPDFKCIPRYYRAGRVOLICPGSAPRSKRSKVKLVSCKKLTFRHNQSEKDF 180
 Db 121 kwwrpngpdfkcipryyragrqlcpqgaaprskrskvilktrfqnqsekd 180
 QY 181 GPETARPQKGRKPRPGARGAKANOLENY 211
 Db 181 gpetarpqkgrkprpgargakangeleny 211
 XX

RESULT 2
 AAY96433 ID AAY96433 standard; Protein; 213 AA. XX
 XX AC AAY96433; XX
 XX DT 12-SEP-2000 (first entry) XX
 XX DE Rat TGF-beta binding protein (BEER). XX
 XX KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein; XX
 XX BBER; gene therapy; antisense therapy; fracture; bone mineralization. XX
 XX OS Rattus norvegicus. XX
 XX WO20032773-A1. XX
 XX PD 08-JUN-2000. XX
 XX PR 24-NOV-1999; 99WO-US27990. XX
 XX PR 27-NOV-1998; 98US-0110283. XX
 XX PA (DARW-) DARWIN DISCOVERY LTD. XX
 XX PR Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW; XX
 XX PI Van Ness J, Winkler DC; XX
 XX PA (DARW-) DARWIN DISCOVERY LTD. DR
 XX WPI: 2000-412321/35.

PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
 PT Van Ness J, Winkler DC;
 XX DR
 PT WPI: 2000-412321/35. XX
 PT N-PSDB: AAA22059. DR
 XX PS Claim 6; Page 125-126; 162pp; English. XX
 XX This shows a rat transforming growth factor beta (TGF-beta) binding protein designated rBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with osteoporosis and fractures. DR
 CC CC inappropriately. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patient's own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content. XX
 CC CC Sequence 213 AA; XX

Query Match 51.2%; Score 108; DB 21; Length 213;
 Best Local Similarity 100 %; Pred. No. 9.6e-104; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX

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 Db 90 tdpcrskakptelvsgqgcpalpnlagnrv 149
 QY 148 GGAPRSKVKLVSCKKLTFRHNQSEKDFGEGTARBEOKRKRPR 195
 Db 150 ggaprskvaklvasckkltfrfqnqsekdkgfpetapqkgrkpr 197
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RESULT 3
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XX AC AAY96434; XX
 XX DT 12-SEP-2000 (first entry) XX
 XX DE Bovine TGF-beta binding protein (BEER). XX
 XX KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein; XX
 XX BEER; gene therapy; antisense therapy; fracture; bone mineralization. XX
 XX OS Bos taurus. XX
 XX PN WO20032773-A1. XX
 XX PD 08-JUN-2000. XX
 XX PR 24-NOV-1999; 99WO-US27990. XX
 XX PR 27-NOV-1998; 98US-0110283. XX
 XX PA (DARW-) DARWIN DISCOVERY LTD. XX
 XX PR Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW; XX
 XX PI Van Ness J, Winkler DC; XX
 XX PA (DARW-) DARWIN DISCOVERY LTD. DR
 XX WPI: 2000-412321/35.

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Run on: November 9, 2001, 15:35:24 ; Search time 47.66 Seconds
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 Gappp 60.0 , gapext 60.0
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 Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
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Post-processing: Listing first 50 summaries

Database : Issued Patents_NA.*

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3	7	3.3	99 4 US-08-370-476-61	Sequence 61, Appl
4	6	2.8	10 1 US-08-250-789A-94	Sequence 94, Appl
5	6	2.8	10 1 US-08-250-789A-95	Sequence 95, Appl
6	6	2.8	10 1 US-08-250-789A-96	Sequence 96, Appl
7	6	2.8	10 1 US-08-333-565-18	Sequence 97, Appl
8	6	2.8	14 1 US-08-333-565-18	Sequence 18, Appl
9	6	2.8	14 2 US-08-661-479-18	Sequence 18, Appl
10	6	2.8	24 1 US-08-220-272A-6	Sequence 6, Appl
11	6	2.8	41 4 US-08-905-223400	Sequence 400, Appl
12	6	2.8	43 2 US-08-488-161-68	Sequence 68, Appl
13	6	2.8	43 3 US-09-273-685-68	Sequence 68, Appl
14	6	2.8	43 5 PCT-0595-1193A-68	Sequence 68, Appl
15	6	2.8	47 2 US-08-281-197C-44	Sequence 44, Appl
16	6	2.8	68 2 US-08-836-791-5	Sequence 5, Appl
17	6	2.8	97 2 US-08-245-511-30	Sequence 30, Appl
18	6	2.8	97 2 US-08-500-993A-30	Sequence 30, Appl
19	6	2.8	125 3 US-08-985-526-25	Sequence 25, Appl
20	6	2.8	128 1 US-08-666-798-2	Sequence 2, Appl
21	6	2.8	128 1 US-08-892-692-2	Sequence 2, Appl
22	6	2.8	128 2 US-09-096-071-2	Sequence 2, Appl
23	6	2.8	167 2 US-08-282-197C-2	Sequence 2, Appl
24	6	2.8	186 4 US-09-475-316A-13	Sequence 13, Appl
25	6	2.8	199 3 US-08-737-248-7	Sequence 7, Appl
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27	6	2.8	204 2 US-08-466-479-2	Sequence 2, Appl

% SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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 6: /cgn2_6/ptodata/2/iaa/backfilesl.pep:*

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Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result and is derived by analysis of the total score distribution

total number of hits satisfying chosen parameters: 212252
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Maximum DB seq length: 30000000

Total number of hits satisfying chosen parameters: 212252

APPENDIX

09-581-10-8

RESULT		1	ALIGNMENTS	
US-08-480-905-61				
Sequence 61, Application US/08484905				
Patent No. 5,97551				
GENERAL INFORMATION:				
APPLICANT: Mottaz, Estelle				
APPLICANT: Abastado, Jean-Pierre				
APPLICANT: Kourilsky, Philippe				
TITLE OF INVENTION: An Altered Major Histocompatibility Antigen Determinant				
TITLE OF INVENTION: Complex (HIC) Determinant a				
TITLE OF INVENTION: Determinant				
NUMBER OF SEQUENCES: 127				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Dunner				
STREET: 1300 T Street, N.W., Suite 700				
CITY: Washington				
STATE: D.C.				
ZIP: 20005-3315				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy Disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: PatentIn Release #1.0, Version #1.				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/484,905				
FILING DATE: 07-JUNE-1995				
CLASSIFICATION: 530				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 07/801,818				
FILING DATE: 05-DEC-1991				
CLASSIFICATION: 530				
ATTORNEY/AGENT INFORMATION:				
NAME: Potter, Jane E. R.				
REGISTRATION NUMBER: 33,332				
REFERENCE/DOCKET NUMBER: 03495.0106-03000				
TELECOMMUNICATION INFORMATION:				
TELEFAX: 202-408-4400				
INFORMATION FOR SEQ ID NO: 61:				
SEQUENCE CHARACTERISTICS:				

RESULT 2
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 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-4841-905-61

RESULT 3
 Query Match 3.3%; Score 7; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

US-08-481-985B-61
 Sequence 61, Application US/08481985B
 Patent No. 601145

GENERAL INFORMATION:
 APPLICANT: Mottez, Estelle
 APPLICANT: Abastado, Jean-Pierre
 APPLICANT: Kourilsky, Philippe
 APPLICANT: Lone, Yu-Chun
 APPLICANT: Ojcius, David
 APPLICANT: Castrouge, Amanda

APPLICANT: Kourilsky, Philippe

APPLICANT: Finnean, Henderson, Farabow, Garrett & D.C.
 ADDRESSEE: Bunner, D.C.
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481, 985B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/792, 473
 FILING DATE: 15-NOV-1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 05243.0001-01000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 99 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-481-985B-61

Query Match 3.3%; Score 7; DB 3; Length 99;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

RESULT 4
 Query Match 3.3%; Score 7; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

Query Match 3.3%; Score 7; DB 70; Length 70;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

Db 64 LLVHAAF 70
 Sequence 61, Application US/08370476
 Patent No. 6153408

GENERAL INFORMATION:
 APPLICANT: Mottez, Estelle
 APPLICANT: Abastado, Jean-Pierre
 APPLICANT: Kourilsky, Philippe
 APPLICANT: Lone, Yu-Chun
 APPLICANT: Ojcius, David
 APPLICANT: Castrouge, Amanda

APPLICANT: Finnean, Henderson, Farabow, Garrett & D.C.
 ADDRESSEE: Bunner, D.C.
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/370, 476
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/117, 575
 FILING DATE: 07-SEP-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/072, 787
 FILING DATE: 06-JUN-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/801, 818
 FILING DATE: 05-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/792, 473
 FILING DATE: 15-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 05243.0001-01000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 99 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-370-476-61

Query Match 3.3%; Score 7; DB 70; Length 70;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

RESULT 4
 Query Match 3.3%; Score 7; DB 70; Length 70;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 MOLECULE TYPE: peptide
 US-08-481-985B-61

Db 64 LLVHAAF 70
 Sequence 94, Application US/08250789A
 Patent No. 5635597

Qy 12 LLVHAAF 18
 |||||

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:47:57 ; Search time 31.03 Seconds

Title: US-09-668-021-14

Perfect score: 213

Sequence: MOLSLAPCLACLVHAAFVA. KPPRPRARGAKANQABLENAY 213

Scoring table: OLI30

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Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEARCHED: 93435 seqs, 34255486 residues

SUMMARIES

ALIGMENTS

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4	8	3.8	850	NRG2_HUMAN
5	7	3.3	97	VE1 HPV4
6	7	3.3	99	B2M_CAVPO
7	7	3.3	110	RL22_ECOLI
8	7	3.3	327	YPER_ECOLI
9	7	3.3	459	TPK_RAT
10	7	3.3	461	TP3K_HUMAN
11	7	3.3	481	LMRA_SRBLN
12	7	3.3	531	TYD2_PARSO
13	7	3.3	547	CAP1_EPHB4
14	7	3.3	632	YGLG_STNV
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16	7	3.3	900	TF2_MYCTU
17	7	3.3	924	IF2_MYCF
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21	6	2.8	65	MLX_KIFP
22	6	2.8	100	VG10_HSEB
23	6	2.8	107	TH12_CORNE
24	6	2.8	110	RL22_ECOLI
25	6	2.8	111	RL22_ACHIL
26	6	2.8	112	RL22_SPCTI
27	6	2.8	113	RL22_THTP
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29	6	2.8	115	TAf_HUMAN
30	6	2.8	115	TAf_MOUSE
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RESULT 1

ELKL_HUMAN

STANDARD: PRT; 428 AA.

P19419; OT5606; O9UM4; 095058; [2]

01-NOV-1990 (Rel. 16; Created)

01-OCT-2000 (Rel. 40; Last sequence update)

01-OCT-2000 (Rel. 40; Last annotation update)

DE ETS-DOMAIN PROTEIN ELK-1.

GN ELK1.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

OX NCBI_TAXID=9606; [1]

RN

SEQUENCE FROM N.A.

MIDDLELINE=89203250; PubMed=2539641; [3]

RA Rac V.N., Huebner K., Isobe M., Al-Rushdi A., Croce C.M., [3]

RA Reddy E.S.P.; [3]

RT 'elk', tissue-specific ets-related genes on chromosomes X and 14 near translocation breakpoints. [3]

RL Science 244:66-70(1989).

RP SEQUENCE FROM N.A.

RX MEDLINE=99013876; PubMed=9795224; [3]

RA Harindranath N., Mills F.C., Mitchell M.P., Meindl A., Max E.E.; [3]

RT The human elk-1 gene family: the functional gene and two processed pseudogenes embedded in the IgH locus. [3]

RT Gene 221:215-224(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Graham D.; [3]

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases. [4]

RN

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA Aryee D.N.T., Kovar H., [3]

RT Novel family members HuER71, ELFP, and ELKv among ETS-related genes coexpressed with EWS-FLI1 in Ewing tumor cell lines. [3]

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases. [5]

RN

RP DOMAINS.

RX MEDLINE=92334979; PubMed=1630903; [3]

RA Janknecht R., Nordheim A.; [3]

RT 'Elk-1' protein domains required for direct and SRF-assisted DNA-binding. [3]

RL Nucleic Acids Res. 20:3137-3124(1992).

CC -1- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM ELEMENT.

CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEAR. [3]

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKv; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: LUNG AND TESTIS.
 CC PMK: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (p38, JNK,
 CC AND ERK).
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC
 DR EMBL; AF00672; AAD0862.1; -.
 DR PIR; AF1351; TWH2K.
 DR HSSP; PI4921; 2STW.
 DR TRANSFAC; T00280; -.
 DR MIM: 311040; -.
 DR InterPro; IPR000418; -.
 DR PRINTS; PRO0454; ETS_DOMAIN.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE; PS00601; ETS_DOMAIN_3; 1.
 KW Transcription regulation; Activator; Nuclear protein; DNA-binding;
 KW Phosphorylation; Alternative splicing;
 DNA_BIND 5 86 VAGCS -> SHCAP (IN ISOFORM 2).
 FT VARSPIC 91 95 MISSING (IN ISOFORM 2).
 FT CONFLICT 183 183 S -> N (IN REF. 1).
 SQ SEQUENCE 428 AA; 44880 MW; 68F718ADB9D38CA CRC64;
 DB 310 PQKGRKPR 317
 RESULT 2
 EELK1_MOUSE STANDARD; PRT; 429 AA.
 AC P19507; 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ETS-DOMAIN PROTEIN EELK-1.
 GN EELK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N_A.
 RN SEQUENCE FROM N_A.
 RC STRAINC57BL/10; TISSUE=Embryo;
 RC MEDLINE=9701716; PubMed=8863747;
 RA Greven D., Ung S., Denhez F., Dehem M., Quattannens B., Begue A.,
 RA Stehelin D., Martin P.,
 RT "Structure and organization of the mouse eelk gene.";
 RT gene 174:185-188(1996).
 RN [2] SEQUENCE OF 5-224 FROM N_A.
 RN TISSUE=Embryo;
 RN MEDLINE=05047310; PubMed=7958835;
 RA Giovane A., Pintas A., Maira S.-M., Sobieszczuk P., Wasyluk B.,
 RA "Net, a new ets transcription factor that is activated by Ras.";

RL Genes Dev. 8:1502-1513(1994).
 CC -!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
 CC SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
 CC FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
 CC ELEMENT.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND TO A
 CC LESSER EXTENT IN THE HEART, LIVER, AND MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X8257; CA60715.1; -.
 DR EMBL; Z36339; CAA8391.1; -.
 DR HSSP; PI4921; 2STW.
 DR MGD; MGI:10183; EELK1.
 DR InterPro; IPR000418; -.
 DR PRINTS; PRO0454; ETS_DOMAIN.
 DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE; PS50081; ETS_DOMAIN_3; 1.
 KW Transcription regulation; Activator; Nuclear protein; DNA-binding;
 KW Phosphorylation;
 DNA_BIND 5 86 ETS DOMAIN.
 FT CONFFLICT 133 133 P -> T (IN REF. 2).
 SQ SEQUENCE 429 AA; 45243 MW; B61B5B97731D54F CRC64;
 DB 311 PQKGRKPR 318
 RESULT 3
 UCR2_HUMAN STANDARD; PRT; 453 AA.
 AC P22695; 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR
 DE (EC 1.10.2.2) (COMPLEX III SUBUNIT II).
 DE UQCRC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N_A.
 RN SEQUENCE FROM N_A.
 RX MEDLINE=9340421; PubMed=2547763;
 RA Hosokawa Y., Suzuki H., Toda H., Nishikimi M., Ozawa T.,
 RT "Complementary DNA encoding core protein II of human mitochondrial
 RT cytochrome bcl complex. Substantial diversity in deduced primary
 RT structure from its yeast counterpart.";
 RL Biol. Chem. 264:13433-13488(1989).
 CC -!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
 CC REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-CL COMPLEX), WHICH
 CC IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THE CORE PROTEIN
 CC 2 IS REQUIRED FOR THE ASSEMBLY OF THE COMPLEX.
 CC 2 FERROCYTOCHROME C.
 CC -!- SUBUNIT: BCL COMPLEX CONTAINS 11 SUBUNITS; 3 RESPIRATORY SUBUNITS

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Om protein - protein search, using sw model

Run on: November 9, 2001, 15:47:20 ; Search time 89.8 Seconds
(without alignments)

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Title: US-09-668-021-14
Perfct score: 213
Sequence: 1 MQLSLAPCLACLLVHAAFAV... KPRPRARGAKANOELENAY 213

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : SPTRREMBL_16:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_micr:*

8: sp_oceanelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	RESULT	1
1	8	3.8	276	13	Q9YGD6	Q9YGD6	PRELIMINARY; PRT; 276 AA.
2	8	3.8	276	13	Q9PT38	Q9PT38	01-MAY-1999 (TREMBLrel. 10, last sequence update)
3	8	3.8	276	13	Q9PT38	Q9PT38	01-MAY-1999 (TREMBLrel. 10, last sequence update)
4	8	3.8	276	13	Q9PT36	Q9PT36	01-MAY-1999 (TREMBLrel. 10, last sequence update)
5	8	3.8	276	13	Q9RDF5	Q9RDF5	01-MAY-1999 (TREMBLrel. 10, last sequence update)
6	7	3.3	499	10	Q9RH55	Q9RH55	01-MAY-1999 (TREMBLrel. 10, last sequence update)
7	7	3.3	109	5	Q9G7J4	Q9G7J4	01-MAY-1999 (TREMBLrel. 10, last sequence update)
8	7	3.3	125	11	Q9BQ01	Q9BQ01	01-MAY-1999 (TREMBLrel. 10, last sequence update)
9	7	3.3	130	2	Q91OC0	Q91OC0	01-MAY-1999 (TREMBLrel. 10, last sequence update)
10	7	3.3	148	2	Q9HVK4	Q9HVK4	01-MAY-1999 (TREMBLrel. 10, last sequence update)
11	7	3.3	150	2	Q9BU66	Q9BU66	01-MAY-1999 (TREMBLrel. 10, last sequence update)
12	7	3.3	151	2	Q9EW14	Q9EW14	01-MAY-1999 (TREMBLrel. 10, last sequence update)
13	7	3.3	151	2	Q9EUV2	Q9EUV2	01-MAY-1999 (TREMBLrel. 10, last sequence update)
14	7	3.3	151	2	Q9EUV1	Q9EUV1	01-MAY-1999 (TREMBLrel. 10, last sequence update)
15	7	3.3	151	2	Q9EUV9	Q9EUV9	01-MAY-1999 (TREMBLrel. 10, last sequence update)
16	7	3.3	151	2	Q9EUV8	Q9EUV8	01-MAY-1999 (TREMBLrel. 10, last sequence update)
17	7	3.3	151	2	Q9EUV7	Q9EUV7	01-MAY-1999 (TREMBLrel. 10, last sequence update)
18	7	3.3	151	2	Q9EUV6	Q9EUV6	01-MAY-1999 (TREMBLrel. 10, last sequence update)
19	7	3.3	151	2	Q9EUV5	Q9EUV5	01-MAY-1999 (TREMBLrel. 10, last sequence update)

SEQUENCE FROM N.A.

Medline-99185307; PubMed-10082666;

RRA Guan G.-J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

RRA "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenases cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss)."; Biochem. Res. Commun. 255:123-128(1999).

RRA -!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY; AF010930; AAD20217.1; -.

RRA EMBL; P20163; 2AEL.

RRA HSSP; P20163; 2AEL.

RRA InterPro; IPR002198; -.

RRA InterPro; IPR002347; -.

RRA PTM; PFO0106; adh_short; 1.

RRA PRMT; PR00081; GDHRD.

RRA PRMTS; PR00080; SDRFAMILY.

RRA KWD; Q9EUV2; -.

RRA Q9EUV1; -.

RRA Q9EUV9; -.

RRA Q9EUV8; -.

RRA Q9EUV7; -.

RRA Q9EUV6; -.

RRA Q9EUV5; -.

RRA Q9EUV4; -.

RRA Q9EUV3; -.

RRA Q9EUV2; -.

RRA Q9EUV1; -.

RRA Q9EUV0; -.

RRA Q9EUX9; -.

RRA Q9EUX8; -.

RRA Q9EUX7; -.

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RRA Q9EUX4; -.

RRA Q9EUX3; -.

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RRA Q9EU20; -.

RRA Q9ETU0; -.

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RRA Q9ETU352; -.

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RRA Q9ETU365; -.

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RRA Q9ETU367; -.

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RRA Q9ETU372; -.

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RRA Q9ETU412; -.

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RRA Q9ETU415; -.

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RRA Q9ETU554; -.

RRA Q9ETU555; -.

RRA Q9ETU556; -.

RRA Q9ETU55

DR	HSSP; P50163; 2AEL.
DR	InterPro; IPR02198; -.
DR	InterPro; IPR02347; -.
DR	Pfam; PF00106; adh.short; 1.
DR	PRINTS; PR00081; GDHR0H.
DR	PRINTS; PR00080; SDRFAMILY.
KW	Oxidoreductase.
SQ	SEQUENCE 276 AA; 30127 MW; 1350E421D34225D CRC64;
RESULT	2
ID	Q9P38
AC	Q9P38;
DT	01-MAY-2000 (TREMBREL; 13, Created)
DT	01-MAR-2001 (TREMBREL; 16, Last annotation update)
DE	CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE A.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TAXID=8022;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-99185307; PubMed=10082666;
RA	Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.: "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";
RT	Biophys. Res. Commun. 255:123-128(1999).
RL	-i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC	EMBL; AF100933; AAD20992.1; -.
DR	DR; P50163; 2AEL.
DR	InterPro; IPR002198; -.
DR	InterPro; IPR002347; -.
DR	Pfam; PF00106; adh.short; 1.
DR	PRINTS; PR00081; GDHR0H.
KW	Oxidoreductase.
SQ	SEQUENCE 276 AA; 30239 MW; 134B52054C751C28 CRC64;
Query Match	3.8%; Score 8; DB 13; Length 276;
Best Local Similarity	100.0%; Pred. No. 2.8;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	28 AFKNDATE 35
Db	93 AFKNDATE 100
RESULT	3
ID	Q9P37
AC	Q9P37;
DT	01-MAY-2000 (TREMBREL; 13, Created)
DT	01-MAR-2000 (TREMBREL; 13, Last sequence update)
DE	CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TAXID=8022;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-99185307; PubMed=10082666;
RA	Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.; "Cloning and expression of two carbonyl reductase-like 20beta-hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";
RT	Biophys. Res. Commun. 255:123-128(1999).
RL	-i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC	EMBL; AF100931; AAD2018.1; -.
DR	DR; P50163; 2AEL.
DR	InterPro; IPR002198; -.
DR	InterPro; IPR002347; -.
DR	Pfam; PF00106; adh.short; 1.
DR	PRINTS; PR00081; GDHR0H.
KW	Oxidoreductase.
SQ	SEQUENCE 276 AA; 30139 MW; 135F1711D30086D CRC64;
Query Match	3.8%; Score 8; DB 13; Length 276;
Best Local Similarity	100.0%; Pred. No. 2.8;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	28 AFKNDATE 35
Db	93 AFKNDATE 100
RESULT	5
ID	Q9RDF5
AC	Q9RDF5;
DT	01-MAY-2000 (TREMBREL; 13, Created)
DT	01-MAR-2000 (TREMBREL; 13, Last sequence update)
DE	PROBABLE TRANSMEMBRANE TRANSPORT PROTEIN.
CC	SCC77.03C.
OS	Streptomyces coelicolor.
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
EMBL; AF100932; AAD20591.1; -.	

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:34:31 ; Search time 79.75 Seconds

{without alignments} 161.917 Million cell updates/sec

Title: US-09-668-021-14

Perfom score: 213

Sequence: 1 MQQLAPCLACLLVHAFVA. KPRPAPGAKANQALENNAY 213

Scoring table: OLIGO

gapop 60.0 , gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_0601.*

1: /SIDS8/gcadata/geneseq/geneseq/A11980.DAT;*

2: /SIDS8/gcadata/geneseq/geneseq/A11981.DAT;*

3: /SIDS8/gcadata/geneseq/geneseq/A11982.DAT;*

4: /SIDS8/gcadata/geneseq/geneseq/A11983.DAT;*

5: /SIDS8/gcadata/geneseq/geneseq/A11984.DAT;*

6: /SIDS8/gcadata/geneseq/geneseq/A11985.DAT;*

7: /SIDS8/gcadata/geneseq/geneseq/A11986.DAT;*

8: /SIDS8/gcadata/geneseq/geneseq/A11987.DAT;*

9: /SIDS8/gcadata/geneseq/geneseq/A11989.DAT;*

10: /SIDS8/gcadata/geneseq/geneseq/A11990.DAT;*

11: /SIDS8/gcadata/geneseq/geneseq/A11991.DAT;*

12: /SIDS8/gcadata/geneseq/geneseq/A11992.DAT;*

13: /SIDS8/gcadata/geneseq/geneseq/A11993.DAT;*

15: /SIDS8/gcadata/geneseq/geneseq/A11994.DAT;*

16: /SIDS8/gcadata/geneseq/geneseq/A11995.DAT;*

17: /SIDS8/gcadata/geneseq/geneseq/A11995.DAT;*

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20: /SIDS8/gcadata/geneseq/geneseq/A11999.DAT;*

21: /SIDS8/gcadata/geneseq/geneseq/A12000.DAT;*

22: /SIDS8/gcadata/geneseq/geneseq/A12001.DAT;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	213	100.0	213	Rat TGF-beta bindi
2	108	50.7	211	Murine TGF-beta bindi
3	33	15.5	176	Bovine TGF-beta bindi
4	33	15.5	213	Human DAN/Cerberus
5	33	15.5	213	Human TGF-beta bindi
6	33	15.5	213	Human TGF-beta bindi
7	33	15.5	213	Vertebrate TGF-beta bindi
8	33	15.5	213	Human TGF-beta bindi
9	33	15.5	213	Human secreted protein
10	33	15.5	213	Human DAN/Cerberus
11	7.0	50	20	Human EST score

ALIGNMENTS

RESULT	1
ID	AAV96433
XX	AAV96433 standard; Protein; 213 AA.
AC	AAV96433;
XX	
DT	12-SEP-2000 (first entry)
DE	Rat TGF-beta binding protein (BEER).
XX	
KW	osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
XX	
OS	Rattus norvegicus.
XX	
PN	WO200032773-A1.
XX	
PD	08-JUN-2000.
XX	
PF	24-NOV-1999; 9900-US27990.
XX	
PR	27-NOV-1998; 9800-0110293.
XX	
PA	(DARWIN) DARWIN DISCOVERY LTD.
XX	
PI	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeper BW;
PI	Van Ness J, Winkler DG;
XX	
DR	WPI; 2000-412321/35.

DR N-PSDB; AAA29059.

PT

PR

XX

Run on: November 9, 2001, 15:35:25 ; Search time 47.66 seconds
 (without alignments)
 100.571 Million cell updates/sec

OM protein - protein search, using sw model

title: US-09-668-021-14

perfect score: 213

Sequence: 1 MQLSLAPCLACILVHAAFVA.....KPRPRARGAKANQAELENAY 213

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Search: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB_pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB_pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB_pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB_pep:*

5: /cgn2_6/ptodata/2/iaa/PCUTS_COMB_pep:*

6: /cgn2_6/ptodata/2/iaa/backfile1_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	9	4.2	206	1	US-09-468-847B-2
2	9	4.2	206	1	US-09-468-847B-20
3	9	4.2	206	1	US-09-468-847B-20
4	9	4.2	206	4	US-09-188-930-159
5	8	3.8	647	3	US-09-753-07A-32
6	8	3.8	647	4	US-09-398-98-32
7	7	3.3	99	2	US-09-424-905-61
8	7	3.3	99	3	US-09-421-905B-61
9	7	3.3	99	4	US-09-370-475-61
10	7	3.3	186	4	US-09-475-316A-13
11	7	3.3	861	1	US-09-764-100-24
12	6	2.8	24	1	US-09-220-22A-6
13	6	2.8	46	4	US-09-188-930-162
14	6	2.8	46	4	US-09-188-930-289
15	6	2.8	68	2	US-09-836-791-5
16	6	2.8	97	2	US-09-245-511-30
17	6	2.8	97	2	US-09-600-933A-30
18	6	2.8	125	3	US-09-595-525-25
19	6	2.8	128	1	US-08-666-798-2
20	6	2.8	128	1	US-08-822-692-2
21	6	2.8	128	2	US-09-096-071-2
22	6	2.8	199	3	US-08-737-248-7
23	6	2.8	202	4	US-09-342-084-10
24	6	2.8	207	4	US-08-652-877-13
25	6	2.8	207	4	US-08-476-515A-13
26	6	2.8	215	3	US-08-462-778-2
27	6	2.8	216	2	US-08-821-637-3

RESULT 1

US-08-468-847B-2

Sequence 2, Application US/08468847B

Patent No. 5780263

GENERAL INFORMATION:

APPLICANT: Hastings, Gregg A. and Adams, Mark D.

TITLE OF INVENTION: Human CCN-Like Growth Factor

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,847B

FILING DATE: 6 June 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-442

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-468-847B-2

Query Match 4.2%; Score 9; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 TITLE OF INVENTION: Human CCN-Like Growth Factor
 NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,847B
 FILING DATE: 6 June 1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-442

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 205 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLogy: LINEAR
 MOLECULE TYPE: PROTEIN

RESULT 2
 US-08-468-847B-20
 ; Sequence 20, Application US/08468847B
 ; Patent No. 578053

GENERAL INFORMATION:
 APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 TITLE OF INVENTION: Human CCN-Like Growth Factor
 NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,847B
 FILING DATE: 6 June 1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-442

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 205 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLogy: LINEAR
 MOLECULE TYPE: PROTEIN

RESULT 4
 US-09-188-930-286
 ; Sequence 286, Application US/09188930A
 ; Patent No. 61,0502

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg
 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 NUMBER OF INVENTION: and Methods For Their Use

CURRENT APPLICATION NUMBER: US/09/188,930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348

SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206

TYPE: PRT
 ORGANISM: mouse

RESULT 4
 US-09-188-930-286
 ; Sequence 286, Application US/09188930A
 ; Patent No. 61,0502

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg
 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 NUMBER OF INVENTION: and Methods For Their Use

CURRENT APPLICATION NUMBER: US/09/188,930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348

SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 286
 LENGTH: 206

TYPE: PRT
 ORGANISM: mouse

RESULT 5
 US-08-53-007A-32
 ; Sequence 32, Application US/08753007A
 ; Patent No. 6074841

GENERAL INFORMATION:
 APPLICANT: Gearing, David P.
 APPLICANT: Busfield, Samantha J.
 TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

RESULT 3
 US-09-188-930-159
 ; Sequence 159, Application US/09188930A
 ; Patent No. 615052

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg

RESULT 3
 US-08-468-847B-20
 ; Sequence 20, Application US/08468847B
 ; Patent No. 578053

GENERAL INFORMATION:
 APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 TITLE OF INVENTION: Human CCN-Like Growth Factor
 NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
 ADDRESS: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

RESULT 3
 US-09-188-930-159
 ; Sequence 159, Application US/09188930A
 ; Patent No. 615052

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg

GenCore - version 4.5
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OM protein - protein search, using sw model

Run on: November 9, 2001, 15:36:30 ; Search time 54.37 Seconds
(without alignments)

245.583 Million cell updates/sec

Title: US-09-668-021-16
Perfect score: 176
Sequence: 1 NDATEIPELGPYPERLPEL... RPQTGKRLPRARGKASRA 176
Scoring table: ORIGO
Gapop 60.0 , Gapext 60.0
Word size : 0
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : PIR.68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7	4.0	119	2 S14292 transcription activator - <i>Emericella nidulans</i>
2	7	4.0	130	2 DB3305 hypothetical proteo
3	7	4.0	139	2 A83305 conserved hypothet
4	7	4.0	148	2 C83091 hypothetical proteo
5	7	4.0	183	2 B37410 H-2 Class II histo
6	7	4.0	230	2 T37095 gene 2.19 protein
7	7	4.0	321	2 B8892 conserved hypothet
8	7	4.0	325	2 T35023 probable secreted
9	7	4.0	328	2 S72547 hypothetical proteo
10	7	4.0	341	2 S71223 xyloglucan endo-1,
11	7	4.0	343	2 B86446 probable endoxylan
12	7	4.0	398	1 S24802 polyferredoxin 6x2
13	7	4.0	426	2 T15285 hypothetical proteo
14	7	4.0	521	2 S24266 glyccoprotein 9C -
15	7	4.0	562	2 T07578 hypothetical proteo
16	7	4.0	573	2 B70942 hypothetical proteo
17	7	4.0	632	1 VGNSY surface glycoprote
18	7	4.0	864	2 JS076 regulatory protein
19	7	4.0	868	1 MAXIC myosin heavy chain
20	7	4.0	1308	1 T15280 hypothetical proteo
21	7	4.0	1646	2 T40198 hypothetical SPC3
22	7	4.0	3006	2 T38625 variant-specific s
23	7	4.0	6420	2 T30283 polyketide synthas
24	6	3.4	49	2 S22125 neurotoxin Tx2 - S
25	6	3.4	65	2 B25025 m6X protein - Kle
26	6	3.4	83	2 S41672 tightly associated
27	6	3.4	89	2 D75271 hypothetical proteo
28	6	3.4	99	2 T17268 probable ribosomal
29	6	3.4	105	2 H72708

ALIGNMENTS

30 6 3.4 106 2 A82560 50S ribosomal prot
31 6 3.4 110 1 R5EC22 ribosomal protein
32 6 3.4 110 2 H85996 50S ribosomal subu
33 6 3.4 111 2 C41839 ribosomal protein
34 6 3.4 113 2 S66512 ribosomal protein
35 6 3.4 118 2 T15239 ribosomal protein
36 6 3.4 119 2 JH0809 hypothetical proteo
37 6 3.4 124 1 R3EC12 lambda 208 protein
38 6 3.4 124 2 JH0443 ribosomal protein
39 6 3.4 124 2 E85998 30S ribosomal subu
40 6 3.4 124 4 JH0807 ribosomal protein
41 6 3.4 124 4 JH0809 ribosomal protein
42 6 3.4 125 2 T10936 cellulase (EC 3.2.
43 6 3.4 129 2 T46388 hypothetical proteo
44 6 3.4 130 2 E82647 hypothetical proteo
45 6 3.4 134 2 D75534 ribosomal protein
46 6 3.4 136 2 T45360 hypothetical proteo
47 6 3.4 137 2 PC4297 cathein F11 - hu
48 6 3.4 141 2 B81268 50S ribosomal prot
49 6 3.4 142 2 H72600 hypothetical proteo
50 6 3.4 145 2 G69011 hypothetical proteo

Query Match 4.0%; Score 7; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 KVRLVAS 133
 Db 12 KVRLVAS 18

RESULT 3
 R8230
 conserved hypothetical protein **WC0373** [imported] - *Vibrio cholerae* (strain NI6961 serogroup O1; Accession: A8230)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B37410
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Yamaishiyan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833
 A:Accession: A8230
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-139 <HEI>
 A:Cross-references: experimental source: serogroup O1; strain NI6961; biotype El Tor
 C:Genetics:
 A:Gene: V0373
 A:Map position: 1
 C:Superfamily: hypothetical protein MJ1081

Query Match 4.0%; Score 7; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 LRPARG 170
 Db 9 LRPARG 15

RESULT 4
 C83091
 hypothetical protein **PA441** [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C83091
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizouchi, S.D.; Warrener, P.; Hickey, M.J.; Brudman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen; Reference number: A82950; MUID:20437337
 A:Accession: C83091
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-148 <STO>
 A:Cross-references: GB:AE004858; GB:AB004091; NID:99950668; PIDN:AA07829; 1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA441

Query Match 4.0%; Score 7; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 ARLLPNA 87
 Db 26 ARLLPNA 32

RESULT 5
 R82892
 conserved hypothetical protein **uW417** [imported] - *Ureaplasma urealyticum*
 C:Species: *Ureaplasma urealyticum*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: B37410
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 A:Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a submitted to GenBank, February 2000
 A:Reference number: A82870
 A:Accession: B37410
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <ELA>

copyright (c) 1993 - 2000 Compugen Ltd.	Gencore version 4.5									
Run on:	November 9, 2001, 15:47:58 ; Search time 31.03 Seconds									
OM protein - protein search, using sw model	(without alignments)									
Title:	US-09-668-021-16									
Perfect score:	176									
Sequence:	I NDATETIPELGEYPEPPLPEL. R P O T G R K L R P R A R G T K A S R A 176									
Scoring table:	OLIGO									
Gapop 60.0 , Gapext 60.0										
Word size :	93435 seqs, 34255486 residues									
Word size :	0									
Total number of hits satisfying chosen parameters:	93435									
Minimum DB seq length:	0									
Maximum DB seq length:	2000000000									
Post-processing:	Listing first 50 summaries									
Database :	SwissProt_39.*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query	Length	DB	ID	Description	RESULT	1		
1	7	4.0	110	1	RL22_LEPIN	Q94d31 leptospira	RL22_LEPIN			
2	7	4.0	230	1	219_HUMAN	P98173 homo sapien	STANDARD;			
3	7	4.0	632	1	VGIG_SYN	P21277 sonchus yel	ID			
4	7	4.0	821	1	ALCR_EMENT	P21228 emericella	AC	Q9XD31;		
5	7	4.0	1168	1	MSC_ACACA	P10569 acanthamoeb	DT	30-MAY-2000 (Rel. 39, last sequence update)		
6	6	3.4	49	1	ITX25_PHONI	P24424 phoneutria	DT	30-MAY-2000 (Rel. 39, last annotation update)		
7	6	3.4	65	1	MLXK_KLEIFI	P29852 klebsiella	DE	50S RIBOSOMAL PROTEIN L22.		
8	6	3.4	97	1	VE7_HMV4	Q80914 human papil	GN			
9	6	3.4	105	1	R3J1_ARPE	Q9y0d25 aeropyrum p	RN			
10	6	3.4	110	1	R122_ECOLI	P03423 escherichia	RP			
11	6	3.4	111	1	R122_ACHTL	P04222 achoplasma	RA	SEQUENCE FROM N.A.		
12	6	3.4	112	1	R122_SPICI	P03160 spiroplasma	RZ	MEDLINE-2008835; PubMed=10520683;		
13	6	3.4	113	1	R122_THETH	P08286 thermus aqu	RT	Zuermer R.L., Hartkekeel R.A., van de Kemp H., Bal A.E.;		
14	6	3.4	115	1	TIAF_HUMAN	Q95411 homo sapien	RT	"Characterization of the Leptospira interrogans S10-spc-alpha		
15	6	3.4	115	1	TIAF_MOUSE	Q95154 mus musculus	RT	RL operon";		
16	6	3.4	118	1	REV_HVILW	Q07624 human immun	RT	FEMS Microbiol. Lett. 182:303-308(2000).		
17	6	3.4	119	1	Y13K_NPVP	Q05122 orgyia pseu	RT	-I- FUNCTION: THIS PROTEIN BELONGS TO 23S RNA; ITS BINDING		
18	6	3.4	123	1	R512_ECOLI	P02367 escherichia	RT	IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND L20.		
19	6	3.4	131	1	RL22_PHYSI	P06094 phoneutria	RT	IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION		
20	6	3.4	148	1	RL22_MAIZE	P06589 zea mays (m	RT	-I- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.		
21	6	3.4	149	1	RK22_ORYZA	P12140 oryza sativ	RT	CC		
22	6	3.4	150	1	R19EL_PYRHO	Q95154 mus musculus	RT	This SWISS-PROT entry is copyright. It is produced through a collaboration		
23	6	3.4	167	1	B3BAR_MERUN	Q07624 human immun	RT	between the Swiss Institute of Bioinformatics and the EMBL outstation.		
24	6	3.4	182	1	YCY0 YEAST	Q05122 orgyia pseu	RT	CC the European Bioinformatics Institute. There are no restrictions on its		
25	6	3.4	184	1	MPL_MPLV	P02367 escherichia	RT	use by non profit institutions as long as its content is in no way		
26	6	3.4	193	1	HS72_CANAL	P06094 phytolasma	RT	modified and this statement is not removed. Usage by and for commercial		
27	6	3.4	196	1	TRPF_KLULA	P06589 zea mays (m	RT	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
28	6	3.4	210	1	DBCL_BACSU	P05041 pyrococcus	RT	or send an email to license@sb-sib.ch);		
29	6	3.4	211	1	REFL_HUMAN	P07432 meriones un	RT	CC		
30	6	3.4	216	1	RGFP_MOUSE	P25654 saccharomyces	RT	EMBL; AF115283; AAC40588.1; .		
31	6	3.4	227	1	PRL_HUMAN	P04931 myeloprolif	RT	DR InterPro: IPR001063; .		
32	6	3.4	227	1	PRL_MACMU	P06589 candida alb	RT	Pfam: PF00237; Ribosomal_L22; 1.		
33	3.4	227	1			P06589 gallus gall	RT	PROSITE: PS0064; RIBOSOMAL_L22; 1.		
						P13997 kluveromyces	RT	Ribosomal Protein; rRNA-binding.		
						P39121 bacillus su	RT	SEQUENCE 110 AA; 12566 MW; B9181B8E9756CAA CRC64;		
						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
						P06589 candida alb	RT			
						P14263 gallus gall	RT			
						P13997 kluveromyces	RT			
						P39121 bacillus su	RT			
						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
						P06589 candida alb	RT			
						P14263 gallus gall	RT			
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						P39121 bacillus su	RT			
						P02528 saccharomyces	RT			
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						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
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						P39121 bacillus su	RT			
						P02528 saccharomyces	RT			
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						P14263 gallus gall	RT			
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						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
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						P02528 saccharomyces	RT			
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						P14263 gallus gall	RT			
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						P04931 myeloprolif	RT			
						P06589 candida alb	RT			
						P14263 gallus gall	RT			
						P13997 kluveromyces	RT			
						P39121 bacillus su	RT			
						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
						P06589 candida alb	RT			
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						P39121 bacillus su	RT			
						P02528 saccharomyces	RT			
						P04931 myeloprolif	RT			
						P06589 candida alb	RT			
						P14263 gallus gall	RT			
						P13997 kluveromyces	RT			
						P39121 bacillus su	RT			

RESULT	2
219_HUMAN	STANDARD; PRT; 230 AA.
ID	219_HUMAN
AC	P98173; F98173;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-2000 (Rel. 40, Last sequence update)
DR	2-19 OR 2-19
DE	2-19 PROTEIN PRBCURSOR.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX	NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Fetal brain;
RX	MEDLINE=94068521; PubMed=8248200;
RA	Bione S., Tamaini F., Meistrini E., Tribolli C., Poustka A., Torri G., Rivello S., Tonolo D.;
RT	"Transcriptional organization of a 450-kb region of the human X chromosome in Xq28.";
RT	Proc. Natl. Acad. Sci. U.S.A. 90:10977-10981(1993).
RP	[2]
RP	SEQUENCE FROM N.A.
RA	Zollo M., Mazzarella R., Bione S., Tonolo D., Schlessinger D., D'Urso M., Chen E.Y., Chen C.-N., RA
RL	Submitted (May-1991) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RX	Pubmed=8733135;
RA	Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N., D'Urso M., Heiner C., Burrough F.W., Ripetto M., Schlessinger D., RA
RT	"Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and GPPD loci.";
RT	Hum. Mol. Genet. 5:659-666(1996).
CC	-1- TISSUE SPECIFICITY: IN SIMILAR AMOUNTS IN TESTIS, PANCREAS, ADRENAL, PLACENTA, BRAIN, FETAL BRAIN, LIVER, KIDNEY, SKELETAL, MUSCLE, HEART.
CC	-1- SIMILARITY: BELONGS TO THE 2-19 FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-
CC	DR
CC	EMBL; L32603; AAA5084.1; -
CC	DR
CC	EMBL; M73626; AAA7890.1; -
CC	DR
CC	PIR; AA0776; VGVNSV.
CC	KW
CC	Transmembrane; Envelope protein; Glycoprotein; Signal.
FT	SIGNAL 1 17 POTENTIAL.
FT	CHAIN 18 632 SPIKE GLYCOPROTEIN.
FT	TRANSMEM 560 578 POTENTIAL.
FT	CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 512 512 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 632 AA: 71093 MW: 05541E78EEA07927 CRC64;
Query Match	4.0%; Score 7; DB 1; Length 632;
Best Local Similarity	100.0%; Pred. No. 14;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	EMBL; X87193; CA60645.1; -
KW	EMBL; L44140; AAA92652.1; -
FT	SIGNAL 1 33 POTENTIAL.
FT	CHAIN 34 230 AA: 25069 MW: FE3334D91F98CAAD CRC64;
SQ	SEQUENCE 230 AA: 585
RESULT	4
ALCR_EMEMI	STANDARD; PRT; 821 AA.
ID	ALCR_EMEMI
AC	P21228; P21228;
DT	01-MAY-1991 (Rel. 18, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	REGULATORY PROTEIN ALCR.
GN	ALCR.
OS	Emericella nidulans (Aspergillus nidulans).
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC	Eurotiales; Trichocomaceae; Emericella.
OX	NCBI_TAXID=5072;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89211976; PubMed=3072264;

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5			
Run on: November 9, 2001, 15:47:21 ; Search time 89.8 seconds				
Scoring table: OLIGO	(without alignments)			
Word size : 0	259.306 Million cell updates/sec			
Searched: 425026 seqs, 132305027 residues				
Total number of hits satisfying chosen parameters: 425026				
Minimum DB seq length: 0				
Maximum DB seq length: 200000000				
Post-processing: Listing first 50 summaries				
Database : SPTRMBL_16:*				
1: sp_archea:*				
2: sp_bacteria:*				
3: sp_fungi:*				
4: sp_human:*				
5: sp_invertebrate:*				
6: sp_mammal:*				
7: sp_mhc:*				
8: sp_orcanelle:*				
9: sp_phage:*				
10: sp_plant:*				
11: sp_rabbit:*				
12: sp_unclassified:*				
13: sp_vertebrate:*				
14: sp_virus:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	7	4.0	45	4 Q9HC30
2	7	4.0	89	10 Q9PH55
3	7	4.0	106	14 Q9IGW4
4	7	4.0	109	5 Q9G7J4
5	7	4.0	130	2 Q91OC0
6	7	4.0	139	2 Q9KUYS
7	7	4.0	148	2 Q9HVK4
8	7	4.0	154	9 Q91999
9	7	4.0	183	7 Q31243
10	7	4.0	220	2 Q9RY8
11	7	4.0	239	14 Q9IBJ1
12	7	4.0	282	10 Q9KF19
13	7	4.0	321	2 Q9PQ72
14	7	4.0	325	2 Q9XAM5
15	7	4.0	341	10 Q38908
16	7	4.0	343	10 Q9FVR2
17	7	4.0	362	2 Q9RJX3
18	7	4.0	398	1 Q00388
19	7	4.0	425	5 Q93348
ALIGNMENTS				
RESULT 1				
Q9HC30	PRELIMINARY;			
Q9HC30;	PRT; 45 AA.			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				
DE CAMP SPECIFIC PHOSPHODIESTERASE VARIANT PDE4A-10 (FRAGMENT).				
GN PDE4A.				
OC Homo sapiens (Human).				
OS Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI-TaxID=9606;				
RN (1)				
RP SEQUENCE FROM N.A.				
RA Sullivan M., Rena G., Begg F., Olsen A.S., Houslay M.D.;				
RT "PDEA-10, a novel human 5' splice variant of the CAMP specific phosphodiesterase PDE4 gene";				
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.				
RL DR EMBL; AEL78570; AAG13806.1; -.				
FT NON_TER 45				
SQ SEQUENCE 45 AA; 4887 MW; A9R65DE550D1283D CRC64;				
Query Match 4.0%; Score 7; DB 4; Length 45;				
Best Local Similarity 100.0%; Pred. No. 6; 3; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Q9FH55 ID Q9FH55 PRELIMINARY; PRT; 89 AA.				
AC Q9FH55;				

GenCore - version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:34:32 ; search time 79.75 Seconds
 (without alignments) 133.791 Million cell updates/sec

Title: US-09-668-021-16
 Perfect score: 176
 Sequence: 1 NDATEIIPELSEYPEPLPEL..... RPQTQTRKLRPARGIKASRA 176

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Search size : 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_0601:*

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2: /SIBS8/gcdata/geneseq/geneseq/geneseq/AA1981.DAT:*

3: /SIBS8/gcdata/geneseq/geneseq/geneseq/AA1982.DAT:*

4: /SIBS8/gcdata/geneseq/geneseq/geneseq/AA1983.DAT:*

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20: /SIBS8/gcdata/geneseq/geneseq/AA2000.DAT:*

21: /SIBS8/gcdata/geneseq/geneseq/AA2001.DAT:*

22: /SIBS8/gcdata/geneseq/geneseq/AA2009

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best result, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description
 1 176 100.0 176 21 AAY96434 Bovine TGF-beta bi
 2 115 65.3 213 21 AAY96431 Vervet TGF-beta bi
 3 76 43.2 213 21 AAB26106 Human DAN/Cerberus
 4 76 43.2 213 21 AAY96429 Human TGF-beta bin
 5 76 43.2 213 21 AAY96430 Human TGF-beta bin
 6 76 43.2 213 21 AAY96436 Human TGF-beta bin
 7 76 43.2 213 21 AAY97589 Human secreted pro
 8 76 367 21 AAB26105 Human DAN/Cerberus
 9 33 18.8 213 21 AAY96433 Rat TGF-beta bindi
 10 32 18.2 211 21 AAY96432 Murine TGF-beta bindi
 11 16 9.1 50 20 AAY12009 Human 5' EST secre

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	176	100.0	176	21	AAY96434	RESULT 1 ID AAY96434 standard; protein; 176 AA. AC AAY96434; XX DT 12-SEP-2000 (first entry) DE Bovine TGF-beta binding protein (BEER). KW osteopathic; transforming growth factor-beta; tgf-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization. KW OS Bos taurus. XX PN WO200032773-A1.
					XX	PD 08-JUN-2000.
					XX	PF 24-NOV-1999; 99WO-US27990.
					XX	PR 27-NOV-1998; 98US-0110283.
					XX	(DARW-) DARWIN DISCOVERY LTD.
					XX	PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paeber BW;
					XX	PI Van Ness J, Winkler DG;
					DR	WPI; 2000-412321/35.

12	7	4.0	219	21	AAG42285	Arabidopsis thalia
13	7	4.0	230	21	AAY57845	Human cytokine fam
14	7	4.0	264	21	AAG15729	Arabidopsis thalia
15	7	4.0	265	21	AAG42284	Arabidopsis thalia
16	7	4.0	273	21	AAG15728	Arabidopsis thalia
17	7	4.0	282	21	AAG42283	Arabidopsis thalia
18	7	4.0	311	22	AAB62150	P. falciplum varC
19	7	4.0	343	21	AAG15727	Arabidopsis thalia
20	6	3.4	12	10	AAP50474	Determinant site O
21	6	3.4	12	10	AAP2004	Human prolactin C-
22	6	3.4	13	7	AAP67042	Sequence from synt
23	6	3.4	20	13	AR27052	N-terminal prolat
24	6	3.4	26	20	AAY16466	SEQ ID NO 364 from
25	6	3.4	29	19	AAY21475	Human neuroendocr
26	6	3.4	44	19	AAM69242	Clone BY6_1 prote
27	6	3.4	44	20	AAW74042	Human D2H binding
28	6	3.4	45	21	AAB38165	Human secreted pro
29	6	3.4	46	21	AAB54384	Human pancreatic
30	6	3.4	50	20	AAY30853	Human secreted pro
31	6	3.4	53	21	AAG01311	Human secreted pro
32	6	3.4	54	21	AAG41013	Zea mays protein f
33	6	3.4	55	21	AAB4093	Human ORFX ORF707
34	6	3.4	59	22	AAB87776	Human T2R46 amino
35	6	3.4	64	21	AAG03123	Human secreted pro
36	6	3.4	68	17	AAR95687	Human GAP-SH3 doma
37	6	3.4	69	21	ARG13973	Arabidopsis thalia
38	6	3.4	70	21	AAG13972	Arabidopsis thalia
39	6	3.4	73	21	AAB5618	Helicobacter pylor
40	6	3.4	74	21	ARG1051	Zea mays protein f
41	6	3.4	79	20	AYY73911	Human prostate tum
42	6	3.4	83	21	AYY52138	Human TANGO 125a (
43	6	3.4	85	21	AYY74211	Human prostate tum
44	6	3.4	87	20	AYY59909	Human normal paner
45	6	3.4	89	21	AAB51453	Human secreted pro
46	6	3.4	91	21	AAB51455	Arabidopsis thalia
47	6	3.4	95	21	ARG13971	Arabidopsis thalia
48	6	3.4	99	21	AYY70744	PSBQ-2 protein enc
49	6	3.4	109	21	AAY96625	Zea mays protein f
50	6	3.4	110	21	AB16029	E. coli proliferat

ALIGNMENTS

DR N-PSDB; AAA29060.

XX Nucleic acids (1) encoding a transforming growth factor beta binding

PT protein, useful for identifying agents for treating osteopenia,

PT osteoporosis and fractures

XX

PS Claim 7; Page 127: 162pp; English.

XX

CC This shows a bovine transforming growth factor-beta (TGF-beta) binding protein designated bBER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with CC inappropriate bBER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or CC vectors may be administered to treat diseases by rectifying mutations or CC deletions in a patient's genome that affect the activity of bBER by CC expressing inactive proteins or to supplement the patient's own production CC of bBER polypeptides. The nucleic acids may be used for recombinant CC production of bBER, gene therapy, antisense therapy, as probes for CC diagnostic assays and for functional studies. bBER may be used to raise CC antibodies and for identification of bBER modulators. bBER antagonists CC may be used to increase bone mineral content for the treatment of CC disorders such as osteopenia, osteoporosis, fractures and other disorders CC associated with low mineral content.

XX

SQ Sequence 176 AA;

Query Match 100.0%; Score 176; DB 21; Length 176;

Best Local Similarity 100.0%; Pred. No. 1. 4e-174; Mismatches 0; Indels 0; Gaps 0;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1 NDATEIPIEGERPERIPELLENKNTMRAENGRGRPHPHPFERKDASEYSCRELHFTRYVTD 60

Db 1 ndateiipegeyapepllelnnkntmraenqgrphphfekdaseyscrelhfyted 60

QY 61 GPCISAKPVTELYCSGOCGPARLPLNAIGRKWWRSGPDRCPIDRYRQRVOLICPG 120

Db 61 gpcisakpvteleycsgocgparlplnaigrkwkwrbsgpdrciparyraqvqlicpg 120

QY 121 AAPRKVYLAVACKELTRPHNOSEIKDGPPEARPQTCRKPRAKRTAKSA 176

Db 121 aaprkvylavackeltrphnoseikdgppearpqtcrkprakrtaksa 176

RESULT 2

ID AAY96431 standard; Protein; 213 AA.

XX

AC AAY96431;

CC 12-SEP-2000 (first entry)

DE Vervet TGF-beta binding protein (bBER).

XX

KW osteopathic; transforming growth factor-beta; TGF-beta; binding protein; KW gene therapy; antisense therapy; fracture; bone mineralization.

OS Cercopithecus pygerythrus.

XX

PN WO20032273-A1.

XX

PD 08-JUN-2000.

XX

PP 24-NOV-1999; 99WO-US27990.

XX

PR 27-NOV-1998; 98US-0110283.

XX

PA (DARWIN) DARWIN DISCOVERY LTD.

XX

PT Brunckow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepke BW;

PT Van Ness J, Winkler DG;

XX

WPI; 2000-412321/35.

DR N-PSDB; AAA29057.

XX Nucleic acids (1) encoding a transforming growth factor beta binding

PT protein, useful for identifying agents for treating osteopenia,

PT osteoporosis and fractures

XX

PS Claim 4; Page 122-123; 162pp; English.

XX

CC This shows a ververt transforming growth factor-beta (TGF-beta) binding protein designated vBER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with CC inappropriate bBER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or CC vectors may be administered to treat diseases by rectifying mutations or CC deletions in a patient's genome that affect the activity of bBER by CC expressing inactive proteins or to supplement the patient's own production CC of bBER polypeptides. The nucleic acids may be used for recombinant CC production of bBER, gene therapy, antisense therapy, as probes for CC diagnostic assays and for functional studies. bBER may be used to raise CC antibodies and for identification of bBER modulators. bBER antagonists CC may be used to increase bone mineral content for the treatment of CC disorders such as osteopenia, osteoporosis, fractures and other disorders CC associated with low mineral content.

XX

SQ Sequence 213 AA;

Query Match 65.3%; Score 115; DB 21; Length 213;

Best Local Similarity 100.0%; Pred. No. 3e-111; Mismatches 0; Indels 0; Gaps 0;

Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 45 SEYSCRLEHFTRYVTDGPCISAKPVTELYCSGOCGPARLPLNAIGRKWWRSGPDRCT 104

Db 76 seyscrelhfytdgpcisakpvteleycsgocgparlplnaigrkwkwrbsgpdrct 135

QY 105 FDYRQRVOLICPGAAPKRKYLVALVACKELTRPHNOSEIKDGPPEARPQ 159

Db 136 pdyrqrqlcpgaaapkarkylvalvackeltrphnoseikdgppearpq 190

RESULT 3

ID AAB26106 standard; Protein; 213 AA.

XX

AAB26106;

XX

DT 15-JAN-2001 (first entry)

XX

DE Human DNA/Cerberus-related protein 6 (hDCR6) (exons 1 and 4).

XX

KW Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein; KW antagonist; BMP; cell growth; cell differentiation; bone formation; KW gene therapy.

XX

OS Homo sapiens.

XX

WO20032273-A2.

XX

PD 21-SEP-2000.

XX

PF 02-MAR-2000; 2000WO-US05537.

XX

PR 12-MAR-1999; 99US-0124118.

XX

PA (REGE-) REGENERON PHARM INC.

XX

PT Economides AN;

XX

WPI; 2000-538179/61.

DR N-PSDB; AAA94051.

XX Novel isolated, human DNA/Cerberus related protein 6 which include PT natural homologue, and polypeptides comprising DCR6 domain and nucleic

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: November 9, 2001, 15:35:25 ; Search time 47.66 Seconds
(without alignments)

83.101 Million cell updates/sec

Title: US-09-668-021-16

Perfect score: 176

Sequence: 1 NDATEIIPPELGEYPEPPLPEL.....RPQTGKLRPRAKGTKASRA 176

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_AAI:*

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3: /cgn2_5/ptodata/2/1aa/5A_COMBO.pep:*

4: /cgn2_5/ptodata/2/1aa/6A_COMBO.pep:*

5: /cgn2_5/ptodata/2/1aa/6CPTUS_COMBO.pep:*

6: /cgn2_5/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	7	4.0	855	4	US-09-813-819-2		Sequence 1, Appli
2	6	3.4	32	2	US-08-078-311-25		Sequence 2, Appli
3	6	3.4	32	2	US-08-460-402-25		Sequence 3, Appli
4	6	3.4	45	2	US-08-078-311-10		Sequence 4, Appli
5	6	3.4	45	2	US-08-460-402-10		Sequence 5, Appli
6	6	3.4	68	2	US-08-836-791-5		Sequence 6, Appli
7	6	3.4	125	3	US-08-985-526-25		Sequence 7, Appli
8	6	3.4	128	1	US-08-985-526-25		Sequence 8, Appli
9	6	3.4	128	1	US-08-892-692-2		Sequence 9, Appli
10	6	3.4	128	1	US-09-096-071-2		Sequence 10, Appli
11	6	3.4	184	2	US-08-078-311-4		Sequence 11, Appli
12	6	3.4	184	2	US-08-460-402-4		Sequence 12, Appli
13	6	3.4	199	3	US-08-737-248-7		Sequence 13, Appli
14	6	3.4	202	4	US-08-342-084-10		Sequence 14, Appli
15	6	3.4	205	1	US-08-468-647B-20		Sequence 15, Appli
16	6	3.4	206	1	US-08-468-647B-20		Sequence 16, Appli
17	6	3.4	206	4	US-09-188-930-159		Sequence 17, Appli
18	6	3.4	206	4	US-09-188-930-286		Sequence 18, Appli
19	6	3.4	216	2	US-08-821-637-3		Sequence 19, Appli
20	6	3.4	223	4	US-08-928-5941D-22		Sequence 20, Appli
21	6	3.4	223	4	US-08-280-5941D-22		Sequence 21, Appli
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23	6	3.4	248	2	US-08-701-935-3		Sequence 23, Appli
24	6	3.4	248	3	US-08-134-591-3		Sequence 24, Appli
25	6	3.4	251	2	US-08-704-931-4		Sequence 25, Appli
26	6	3.4	253	3	US-08-985-526-27		Sequence 26, Appli
27	6	3.4	254	2	US-08-701-935-6		Sequence 27, Appli

ALIGNMENTS

RESULT 1 US-09-813-819-2

Sequence 2, Application US/09813819

Patent No: 6294368

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND NUCLEIC ACID MOLECULES ENCODING, HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001177

CURRENT APPLICATION NUMBER: US/09/813,819

CURRENT FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 855

TYPE: PRT

ORGANISM: Human

US-09-813-819-2

RESULT 2

Query Match 4.0%; Score 7; DB 4; Length 855;

Best Local Similarity 100.0%; Pred. No. 69; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 ARGTAKAS 174

 |||||||

Db 772 ARGTAKAS 778

RESULT 2

Sequence 25, Application US/08078311

Patent No: 5925750

GENERAL INFORMATION:

APPLICANT: Charon, Martine

APPLICANT: Gisselbrecht, Silvie

APPLICANT: Penczek, Jean-Francois

APPLICANT: Souyri, Michele

APPLICANT: Tambourin, Pierre

APPLICANT: Varlet, Paule

APPLICANT: Vigon, Isabelle

APPLICANT: Wendel, Francoise

TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of

TITLE OF INVENTION: Myeloproliferative Disease
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 3100 No. 592575west Center
 CITY: Minneapolis
 STATE: MN
 ZIP: 55402
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/078,311
 FILING DATE: 18-JUN-1993
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR90/00762
 FILING DATE: 19-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Kowalczyk, Katherine M.
 REGISTRATION NUMBER: 35,848
 REFERENCE/DOCKET NUMBER: 8076,84US03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 CLONE: Extracellular domain of v-mpl
 US-08-078-311-25

RESULT 3
 US-08-460-402-25
 Sequence 25, Application US/08460402
 Patent No. 598983
 GENERAL INFORMATION:
 APPLICANT: Charon, Martine
 APPLICANT: Gisselbrecht, Silvie
 APPLICANT: Pencioelli, Jean-Francios
 APPLICANT: Souyri, Michelle
 APPLICANT: Tambourin, Pierre
 APPLICANT: Varlet, Paule
 APPLICANT: Vigan, Isabelle
 APPLICANT: Wending, Francoise
 TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
 TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
 TITLE OF INVENTION: Myeloproliferative Disease
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 3100 No. 592575west Center
 CITY: Minneapolis
 STATE: MN
 ZIP: 55402
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,402
 FILING DATE:
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/309, 259
 FILING DATE: 20-SEP-1994
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/078, 311
 FILING DATE: 18-JUN-1993
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR90/00762
 FILING DATE: 14-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Randall A. Hillson
 REGISTRATION NUMBER: 31,838
 REFERENCE/DOCKET NUMBER: 8076,84US03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 CLONE: Extracellular domain of v-mpl
 US-08-460-402-25

RESULT 4
 US-08-078-311-10
 Sequence 10, Application US/08078311
 Patent No. 5225750
 GENERAL INFORMATION:
 APPLICANT: Charon, Martine
 APPLICANT: Gisselbrecht, Silvie
 APPLICANT: Pencioelli, Jean-Francios
 APPLICANT: Souyri, Michelle
 APPLICANT: Tambourin, Pierre
 APPLICANT: Varlet, Paule
 APPLICANT: Vigan, Isabelle
 APPLICANT: Wending, Francoise
 TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
 TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
 TITLE OF INVENTION: Myeloproliferative Disease
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 3100 No. 592575west Center
 CITY: Minneapolis
 STATE: MN
 ZIP: 55402
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible